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Db 1 CCACCGGAGGCGCGCGGAAATCATACCGGGGGCGCGCGCTGTGGCATGTGGCTGTG 60
07 61 CCGGAGCATCTCTGGAGCGGCTGTGTAGTGGCTTACTGCATGACCCCGCGACCTTAAACAT 120
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07 121 CAGGAGGAGTGCACAGCTATCATGACACCGGGTGAACCGCTGTCCATCTCTGACGGGACA 180

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QY	1741	GCTCTGAGACTCTCCAAAGCCGACAGACTACAAATACAGAGATCTGCGCTGGTACCGCTCAA	1800
Db	1752	GCTCTGAGACTCTCCAAAGCCGACAGACTACAAAGTACAGAGATCTGCGCTGGTACCGCTCAA	1811
QY	1801	GCTGTCACAGCTGACAGCATGCGCACAGGAAATCCGTTCTGCTGACTCCAAAGACTGCA	1860
Db	1812	CGCTGTCACAGCTGACAGCATGCGCACAGGAAATCCGTTCTGCTGACTCCAAAGACTGCA	1871
QY	1861	TCTGTTCGCTACACCTCTCTGGGCGCGAGCCCTGAGAGAGTGTGACACTGTGAGCGCGCCAGCC	1920
Db	1872	TCTGTTCGCTACACCTCTCTGGGCGCGAGCCCTGAGAGAGTGTGACACTGTGAGCGCGCCAGCC	1931
QY	1921	CAGGCTCAATGAGATATACGATCCGACGCTGGCGCCGACAGACAGGAGCCACTATGTGGCA	1980
Db	1932	CAGGCTCAATGAGATATACGATCCGACGCTGGCGCCGACAGACAGGAGCCACTATGTGGCA	1991
QY	1981	AGTGTCAACACCGGCGACACCCATGACAAAGACTGCGCACAGAAACTACTGTGCGTGCAGCG	2040
Db	1992	AGTGTCAACACCGGCGACACCCATGACAAAGACTGCGCACAGAAACTACTGTGCGTGCAGCG	2051
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Db	2052	CGTGGAGCCCGCTGCGGTCCACATGAGAGACTTGAAGGACTCTGTGTGAGCTGACGACTC	2111
QY	2101	GGTGGAGATGAGAGTCTGTGGTGGCGCGACGACGCGCTGACAGATGGTGGTGGTACAAAGA	2160
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QY	2161	CGAGAGGCTGCTGSAKAAAAAGTCTGAGATGACATCTGAGAGATTCGACACGAGAGCTAG	2220
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QY	2221	CATTCACGCGCGTGGCGGACGAGAGATGCGGCAAGGCTATGTGTGAGTGTGCACGCCAA	2280
Db	2232	CATTCACGCGCGTGGCGGACGAGAGATGCGGCAAGGCTATGTGTGAGTGTGCACGCCAA	2291
QY	2281	GCGCTGCTGCAACTCTGCTGCGCCGACGTGCGCTGTGAATGCTGCGAGAGATTAAGGGAGCAT	2340
Db	2292	GCGCTGCTGCAACTCTGCTGCGCCGACGTGCGCTGTGAATGCTGCGAGAGATTAAGGGAGCAT	2351
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Db	2352	GGAAATCTGATCTTGTGCGTGAAGAGAGCTATGCTGTCTCTCTCTGTGCGTCTCTCTCT	2411
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Db	2412	CGTGTACTCTGTAACTATGAGAGAGCGCGCTGACGACAGATCAATCAACCGGCTACCTCTC	2471
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Db	2472	CATCAATCATGAGCGCGCGGAGAGGCTGTGAGSAGATAGTGGAAATAGCTGTGCTTACGA	2531
QY	2521	TGGCAGCCAGTGGGAAATTCGCCGAGAGAGCGATGCACTGTGGAGAGAGTCTCTGCTTACG	2580
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QY	2641	CAGCGTGGGCGTGAATATGCTGAAGAGAGCGCGACGCGCCAGCGAGACCGCGGCGCTAT	2700
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QY	2701	GTCGAGCTCAAGATCTCTATTTACATGCGGTAACGACTCAAGGTGGTCAACTCTCTCGG	2760
Db	2712	GTCGAGCTCAAGATCTCTATTTACATGCGGTAACGACTCAAGGTGGTCAACTCTCTCGG	2771
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Db	2772	GAGGTGACAGTACCCCGAGAGCGCCCTCAATGCTATGATGAGTGTCTGCAATACCGCAA	2831

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Db	2832	CTCTCTCCAACTTCCTCGCGGCCCAAGGGGAGACGCTTACAGCCCTCGCGGAGAACTCTCC	2891
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Db	2892	CGACAGACGGGAGACCTTCGCGGCACTGGTGGAGGCTCCGACAGGTGGATCGGAGCGCGGC	2951
QY	2941	GGGGAGACGACGACAGGCTCTCTCTCGCGCGCTTCTCGAAGACCCAGGGGCGAGACGAGCGG	3000
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QY	3001	GGCTCTCCAGACCAAGAAAGCTGGAGACCTGTGTGCTGAGCCCGCTGACCTATGAGATCTT	3060
Db	3012	GGCTCTCCAGACCAAGAAAGCTGTGAGACCTGTGTGCTGAGCCCGCTGACCTATGAGATCTT	3071
QY	3061	TGTTCTGCTACACTTCCAGGTGGGCGACAGAGGATGAGATTCTGTGCTTCCGAAAGTGCAT	3120
Db	3072	TGTTCTGCTACACTTCCAGGTGGGCGACAGAGGATGAGATTCTGTGCTTCCGAAAGTGCAT	3131
QY	3121	CCACAGAGACCTTGCTGCTCCGAACATTTCTGTGGGAAACGACGTGTGAGATCTTG	3180
Db	3132	CCACAGAGACCTTGCTGCTCCGAACATTTCTGTGGGAAACGACGTGTGAGATCTTG	3191
QY	3181	TGACTTTGGCCTTGGCGGGACATCTACAAAGCCCTACATAGCTCCGCAAGGGCGCATGCG	3240
Db	3192	TGACTTTGGCCTTGGCGGGACATCTACAAAGCCCTACATAGCTCCGCAAGGGCGCATGCG	3251
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Db	3312	GAGTGACGTGTGTCTCTTGGGGTCTCTCTGGGAGATCTTCTCTCTGTGGGGGCTCTCCG	3371
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 4844 AACGGAGGAGGAGAGCT 4857

RESULT 4
 US-09-982-610-17/c
 Sequence 17, Application US/09982610
 Patent No. US2002014620A1
 GENERAL INFORMATION:
 APPLICANT: Genentech, Inc.
 Inventor: Bennett, Brian D.
 Lee, James M.
 Matthews, William
 Tsai, Siao Ping
 Wood, William I.
 TITLE OF INVENTION: PROTEIN TYROSINE KINASE ANONIST ANTIBODIES
 NUMBER OF SEQUENCES: 45
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Minitab (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/982,610
 FILING DATE: 17-Oct-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/446,648
 FILING DATE: 1996-May-23
 APPLICATION NUMBER: 08/222616
 FILING DATE: 04-APR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Lee, Wendy M.
 REGISTRATION NUMBER: 40,378
 REFERENCE/DOCKET NUMBER: P08218PCT

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-1994
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6827 base pairs
 TYPE: Nucleic Acid
 STRANDEDNESS: Single
 TOPOLOGY: Linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 17:
 US-09-982-610-17

Query Match 25.3% Score 1040.2; DB 10; Length 6827;
 Best Local Similarity 98.3%; Pred.No 7.1e-252;
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2357 GTGGAGAGAGAGAGAGAGCTGTGATTCATGAGAGAGAGAGAGAGAGAGAGAGAGAG 2416
2584 GTGGAGAGAGAGAGAGAGCTGTGATTCATGAGAGAGAGAGAGAGAGAGAGAGAGAG 2463
2417 ATGAGAGAGAGAGAGAGCTGTGATTCATGAGAGAGAGAGAGAGAGAGAGAGAGAG 2476
2644 GTTAAAGAGAGAGAGAGAGCTGTGATTCATGAGAGAGAGAGAGAGAGAGAGAGAGAG 2703
2477 GTGGAGAGAGAGAGAGAGCTGTGATTCATGAGAGAGAGAGAGAGAGAGAGAGAGAG 2536
2704 GATGAGAGAGAGAGAGAGCTGTGATTCATGAGAGAGAGAGAGAGAGAGAGAGAGAG 2763
2537 GTGGAGAGAGAGAGAGAGCTGTGATTCATGAGAGAGAGAGAGAGAGAGAGAGAGAG 2596
2764 GTGGAGAGAGAGAGAGAGCTGTGATTCATGAGAGAGAGAGAGAGAGAGAGAGAGAG 2833
2597 GTGGAGAGAGAGAGAGAGCTGTGATTCATGAGAGAGAGAGAGAGAGAGAGAGAGAG 2656

2824 ATTGAGAGAGAGAGAGAGCTGTGATTCATGAGAGAGAGAGAGAGAGAGAGAGAG 2883
2857 ATGCTGAGAGAGAGAGAGAGCTGTGATTCATGAGAGAGAGAGAGAGAGAGAGAGAG 2916
2884 ATGCTGAGAGAGAGAGAGAGCTGTGATTCATGAGAGAGAGAGAGAGAGAGAGAGAG 2943
2717 GTGATTCATGAGAGAGAGAGAGCTGTGATTCATGAGAGAGAGAGAGAGAGAGAGAGAG 2776
2944 GTGATTCATGAGAGAGAGAGAGCTGTGATTCATGAGAGAGAGAGAGAGAGAGAGAGAG 3003
2777 GAG 2836
3004 GAG 3063
2837 GCGGAG 2896
3064 GCGGAG 3123
2897 GTGGAGAGAGAGAGAGAGCTGTGATTCATGAGAGAGAGAGAGAGAGAGAGAGAGAG 2956
3124 AAGAGAGAGAGAGAGAGCTGTGATTCATGAGAGAGAGAGAGAGAGAGAGAGAGAG 3183
2957 GTGGAGAGAGAGAGAGAGCTGTGATTCATGAGAGAGAGAGAGAGAGAGAGAGAGAG 3016
3184 AAGAGAGAGAGAGAGAGCTGTGATTCATGAGAGAGAGAGAGAGAGAGAGAGAGAG 3243
3017 GAGAGAGAGAGAGAGAGCTGTGATTCATGAGAGAGAGAGAGAGAGAGAGAGAGAG 3070
3244 GAGAGAGAGAGAGAGAGCTGTGATTCATGAGAGAGAGAGAGAGAGAGAGAGAGAG 3303
3071 AGCTTCAGAGAGAGAGAGAGCTGTGATTCATGAGAGAGAGAGAGAGAGAGAGAGAG 3130
3304 AGCTTCAGAGAGAGAGAGAGCTGTGATTCATGAGAGAGAGAGAGAGAGAGAGAGAG 3363
3131 GTGGAGAGAGAGAGAGAGCTGTGATTCATGAGAGAGAGAGAGAGAGAGAGAGAGAG 3190
3364 GTGGAGAGAGAGAGAGAGCTGTGATTCATGAGAGAGAGAGAGAGAGAGAGAGAGAG 3423
3191 GTGGAGAGAGAGAGAGAGCTGTGATTCATGAGAGAGAGAGAGAGAGAGAGAGAGAG 3250
3424 GTGGAGAGAGAGAGAGAGCTGTGATTCATGAGAGAGAGAGAGAGAGAGAGAGAGAG 3483
3251 GTGGAGAGAGAGAGAGAGCTGTGATTCATGAGAGAGAGAGAGAGAGAGAGAGAGAG 3310
3484 GTGGAGAGAGAGAGAGAGCTGTGATTCATGAGAGAGAGAGAGAGAGAGAGAGAGAG 3543
3311 GTGGAGAGAGAGAGAGAGCTGTGATTCATGAGAGAGAGAGAGAGAGAGAGAGAGAG 3370
3544 GTGGAGAGAGAGAGAGAGCTGTGATTCATGAGAGAGAGAGAGAGAGAGAGAGAGAG 3603
3371 GTGGAGAGAGAGAGAGAGCTGTGATTCATGAGAGAGAGAGAGAGAGAGAGAGAGAG 3430
3604 GTGGAGAGAGAGAGAGAGCTGTGATTCATGAGAGAGAGAGAGAGAGAGAGAGAGAG 3663
3431 GAG 3490
3664 GAG 3723
3491 GAG 3550
3724 GAG 3783
3551 GTGGAGAGAGAGAGAGAGCTGTGATTCATGAGAGAGAGAGAGAGAGAGAGAGAGAG 3567
3784 GAG 3800

RESULT 6
US-09-919-408-5
; Sequence 5, Application US/09919408
; Patent No. US20020072077A1
; GENERAL INFORMATION:

APPLICANT: Lemischka, Thor R.
TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
RECEPTORS AND THEIR LIGANDS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Imclone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: U.S.A.
Zip: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/919,408
FILING DATE: 31-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/977,451
FILING DATE: <Unknown>
APPLICATION NUMBER: US 07/936,397
FILING DATE: 26-JUN-1992
APPLICATION NUMBER: US PCT/US92/05402
FILING DATE: 25-JUN-1992
APPLICATION NUMBER: TW 8102961
FILING DATE: 15-APR-1992
APPLICATION NUMBER: US PCT/US92/02750
FILING DATE: 02-APR-1992
APPLICATION NUMBER: US 07/813,534
FILING DATE: 24-DEC-1991
APPLICATION NUMBER: US 07/793,065
FILING DATE: 15-NOV-1991
APPLICATION NUMBER: US 07/728,913
FILING DATE: 28-JUN-1992
APPLICATION NUMBER: US 07/679,666
FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Felt, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: IEM-3-7P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 5426 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYDROTHERMAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
FEATURE:
NAME/KEY: CDS
LOCATION: 208..4311
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 265..4308
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 208..264
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-919-408-5
Query Match 17.3%; Score 713; DB 10; Length 5406;
Best Local Similarity 54.5%; Pred. No. 1,36-159;
Matches 1711; Conservative 0; Mismatches 1345; Indels 81; Gaps 11;
QY 464 AACAGCAAGACGATCTGGGCGCCCTGTTCTGCTGATCCGAGGCTCAATGTCAGC 523

DB 634 AACAGCAAAACGATGGTGATCCCTCCGAGGCTGATTTCAACCTCAATGTCAT 693
QY 524 CTGCGC-----TGCAAAGCTGGTGTGCTGCCCACAGCGGACGAGGTGTGGGAT 577
DB 694 CTTTCGGCTAGGATATCCGAAAGAGATTGTGTCCGATGGAACAAAGAAATTTCTGGGAC 753
QY 578 GACGGGGGGGCGATGCTGTGTGTCACCCGACCTGCTGCACGATGCGCTGACTGAGTGC 637
DB 754 AGCGAGATAGCCTTTACTCTCCGAGTACATGATGACGATGAGCGGATGCTTTCTGT 813
QY 638 GAGACCCAGCTGGGAGACGACGACTTCTTTCCAAACCCCTTCTGTGTCATCATCAGGC 697
DB 814 GAGGCAAGATCAATGATGAAACCTTACGTATCATGTCATCATGATGATGATGATGATG 873
QY 698 AACGAGCTCTATGACATCCAGCTGTGCCCAGGAAGTCTGAGAGTCTGTAGGGAG 757
DB 874 TAGAGATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 933
QY 758 AAGCTGTGCTGAGATGACCTGCTGTGCGGCTGATTAATCATGAGTGCACCTTTGACGTG 817
DB 934 AACTTTGCTTAATTTGTATGACGAGACGAGATGAGGCTGATTTACCTG 993
QY 818 GACTACCCAGGGAAGCAGGC-----AGACGGGGTAAAGTGGTGCCGACGACGCT 869
DB 994 CACTCTCCACTCAAGATCTCATCATAGAAAGATTGTAAACGGGATGTAAACCTTT 1053
QY 870 CCGACGACACCCACAGAACTTCC-AGCATCTGACCATCCAAAGCTCAGCCAGCAGC 928
DB 1054 CCTGGCACTGGGGAAGATGTTTGTGACACCTTGACAAATAGAAAGTGTGACCAAGT 1113
QY 929 GACCTGGGCTGTATGTGTGCAAGGCAACAGGCAATCCAGGATTTGGGAGAGCACC 988
DB 1114 GACCAAGGGAAATACCTGTGTAGCGTCAATGACGATGATCAAGAAATGAACA 1173
QY 989 GAGGTGATTTGATGCAAAATCCCTTCATCAGCTGAGTGGCTCAAGAGACCAATCTGTG 1048
DB 1174 TTGTGCGAGATTCACAAAGCCTTTATGTGCTTGTGATGATGATGATGATGATGATG 1233
QY 1049 GAGGCGACGAGAGAGAGAGTGTGAGAGCTGCGCCGTGAAGCTGACAGCTACCCCGG 1108
DB 1234 GAGGCA---CAGTGGGCACTGCAAGTCCGATCTGGAAGTATCTGATTAACCACT 1290
QY 1109 CCGGAGTTCAGTGTGTAAGATGTAAGAGGAGTGTGCGGGGCCACA-----GT 1159
DB 1291 CCGTATATCAATATGTACAAATGGAAGGCCCATTTGATCCAACTACAAATGATTTT 1350
QY 1160 CCACATGCCCTGTGCTCAGAGAGTGAAGAGGCGACACAGGACCTACACCTCTGCC 1219
DB 1351 GCGGATGAATCAGATCATGATGAGAGTGAAGTGAAGAGATGACAGAAATCTACAGGTCTATC 1410
QY 1220 CTGTGAACTCCCTGTGCTGAGCGCCCAACATCAAGCTGAGCTGTGTGTAATGTG 1279
DB 1411 CTCACCAACCCCATTTCAATGAGAAACAGACCAATGATCTCTGTGTGTGAAATGTC 1470
QY 1280 CCCCCCAGATACATGAGAAAGAGGCTCTTCCCA---GCATCTACTCGGCTCACAC 1336
DB 1471 CCACCCAGATCGGTGAGAAAGCCTTGATCTGCTGATGATGATGATGATGATGATG 1530
QY 1337 CCGCAGGCGCTCAGCTGCAAGGCTGAGGAGGCTGCGCTGCTGACATCCAGTGGGAGC 1396
DB 1531 ATGCAAGATTTGACATCAGATGATGAGGCAACCTTCCCTGCAACATCTCAATGATGATG 1590
QY 1397 TGGCGGCGCTGACACCTCTGCAAGATGTTGGCCAGGCTAGTCTCCGGGGGCGGACGAG 1456
DB 1591 TGGCAGGTAGAAAGAGCTGC-----TCTACAGACCCGGGCAAA 1630
QY 1457 CAAGACCTCATCCACAGTCCCTGACTGAGAGGCGGTGACACGACGATGCTCGTGAAC 1516
DB 1631 CAAGCCCTTATGCT---TTGTAAGATGAGACACGTGAGGAGATTTCCAGGGGGAAC 1686
QY 1517 CCGATCGAGACCTGAGACCTGAGACCGGATTTGTGGAGGGAAGAAATGAGACTGTGAGC 1576

[illegible]

OY	2657	AAGCTGAAAGAGGGGGCCACCGGCACGAGACACCGGGCGGTATGTTCGGAGCTCAAAAGTAC	2716
Dd	2806	ATGTGTAAGAAGAGGAACAACACAGCAGACATCACGCCCTCATGTCTGAACTCAAGATTG	2865
OY	2717	CTCATTCACATGCGCCAACACCCTCAACAGTGTCATAACTCTCTCGGGGGGTGCATCCAAAGCGC	2776
Dd	2866	CTCATTCACATTTGGTACACATCTCTAATGTGTGTAACTCTCTTAGGGCGCTGCACCAAAGCGC	2925
OY	2777	CAGGGCCCCCTCATGTGTATCTGTGAGTTCCTGTGCAGTAGGCAACTCTTCCAATTCTGTG	2836
Dd	2926	GGAAGGGCTCTCATGTGATTTGTGAAATCTCGAAATGTGGAAACTATCAACTTACTTA	2985
OY	2837	CGGCGCCACCGGAGACCCCTTACGCCCTTGCGGGGAAGAAAGTCTCCCGAGACGCGCGAGACGC	2896
Dd	2986	CGGGGCAAGAGAAATGAATTTTGTCCTATTAGACCAAAAAGGGGACACGCTTCCGCCAGGCGC	3045
OY	2897	TTCGGGCGCATGTGTGACTTCGCACGCGCTGATCTGGAGCGCGCGGGGACACCGACAGC	2956
Dd	3046	AAGGACTACGTTGGGGAGACTTCCTCGTGTGATCTGTAAACACCCCTTGGACAGCATACACACGC	3105
OY	2957	GTCCTCTTGGCGGGTTCTCGAAGACCGAGGGCGGAGCGAGGCGGGCTTCTCGACACCA	3016
Dd	3106	AGCCAGACCTCTGCCAGCTACGCGCTTGTGTGAGAGAAATCGCTCATGTGATGAGAGAA	3165
OY	3017	GAAAG-----CTGAGAGACTTGTGGCTGAGCGCCCGCTGACCATGTGAAGATCTTGTCTATAC	3070
Dd	3166	GAAAGAACTTCTGTAAAGAACTGTACAGAGATTCCTGACTTGTGAGCATCTCATCTGTATAC	3225
OY	3071	AGCTTCACAGTGGCCACGAGGGATGAGATTCTCTGCGTTCGCCAAGTGCATCCACACAGACAC	3130
Dd	3226	AGCTTCCAAGTGGCTTAAGGGCATGTGAATTTGTGGCATCAAGGAAGTGTATATCCACAGGGAC	3285
OY	3131	CTGGCTGTCTGGACACATTCTCTGTGTGGAAAAAGCAGTGTGTGAAGATCTGTGACTTTGGC	3190
Dd	3286	CTGGCAGCAGCAAAATCTCTCTATCGAGAAAGAAATGTGGTTAAGATCTGTGACTTCGGC	3345
OY	3191	CTTGCCCGGGAGCATATCAAAAGACCCGTGAGCTAGTCCGCAAGGGGCAATGGCCCGGGCTGCC	3250
Dd	3346	TTGCGCCCGGAGATTTATTAAGAGCCCGGATTAATGTACAAAAGAGATGGCCCATCTCCT	3405
OY	3251	CTGACAGTGGATGGCCCTGAAAGCATCTTGTCGACAAAGGTGTACACACAGCAGAGATGACGTG	3310
Dd	3406	TTGAGTGGATGGCCCCGGAACCATTTTTTGAACAGAGTATACACAAATTACAGACGATGTG	3465
OY	3311	TGTCCTTTGGGGTCTTCTCTGTGGAGATCTTCTCTGTGGGGGCGCTCCCGTACCTGGG	3370
Dd	3466	TGCTCTTTCGGTGTCTGTCTGTGTGGAAATAATTTCTTATAGTGGCTCCCATACCTGGGG	3525
OY	3371	GTCGCAATCAATCAACATCTCTGTGACGCGCTGAGAGAGCGCAACAAAGATGAGAGGCGCGG	3430
Dd	3526	GTCAAATTTGATGAAGAAATTTTGTATATATATTAAGAGGAAGACTATCAAAATGTGTGGCTCT	3585
OY	3431	GACCTGGCCACTCCCGCATACGCGCCCATATCATGTGAACTCTGTCTGGGAGACCCCAAG	3490
Dd	3586	GACTACATCAACCCCGAAATGTACACAGACCATGTGTGACTCTGTGGCATGAGACCCCAAC	3645
OY	3491	GCGAGACCTGCAATTCCTGGAGCTGTGTGABATCTCTGGGGGACCTGTCTCAGGGCAAGGGGC	3550
Dd	3646	CAGAGACCTCTCTTTCAGATTGTGTGGAGCATTTGGGAACCTCTCTGCAGCAACAAATGGG	3705
OY	3551	CTTCAGAGAGAGAGAGA 3567	
Dd	3706	CAGCAGGATGACAAAGA 3722	

RESULT 7 -
US-09-872-136-5
Sequence 5, Application US/09872136
Patent No. US2002011945A1
GENERAL INFORMATION:
APPLICANT: Lemischka, Thor R.
TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELLS

QY 758 AAGCTGATCTGAACTGACCGCTGAGGCTGAGTTTAACTGAGGTGCTACCTTTGACTGG 817
DB 721 AAGCTGATCTTAAATGTATGACAGCAAGCACTGAATTAATGTGGGATGACTCTCAACTGG 780
QY 818 GATTAACCAAGGAAAGCAAGCAAGCGGGGTAGTGGGTGCGCCGACAGCGCTCCACGAC 877
DB 781 GAATTAACCTTCTTGAAGCAATCAAGAACTGTAAACCGACACTTAAAAACCCAG 840
QY 878 ACCGACACAG-----AAGTCTCCAGCATCTGACCATCCGACCAACGTCAGCCGAC 928
DB 841 TCTGGAGATGACATGAAAGAAATTTTGGACCACTTAATTAATAGTGTGTGAACCCGCACT 900
QY 929 GACCTGGGCTGCTATGATGTGCAAGGCCAACCAAGGCATTCAGCATTTCCGGAGACAC 988
DB 901 GACCAAGGATTTTAACTGTGACCATCCAGTGGGTGTATGACCAAGAAAGAACGACAA 960
QY 969 GAGTCATTTGCAATGAAATCCCTTCAATCAAGTGTGAGTGGCTCAAGAGACCATCTG 1048
DB 961 TTGTCAGGATGCAATGAAATCCCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1020
QY 1049 GAAGCTAAGGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1108
DB 1021 GAAGCAAGGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1077
QY 1109 CCGGATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1159
DB 1078 CCAAAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1137
QY 1160 CAGCATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1219
DB 1138 GAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1197
QY 1220 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1279
DB 1198 CTTACCAATCCCATTTCAAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1257
QY 1280 CCGCCCAAGATACATGAG 1339
DB 1258 CCAAGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1317
QY 1340 CAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1396
DB 1318 ACTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1377
QY 1397 GAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1456
DB 1378 GAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1426
QY 1457 GAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1516
DB 1427 GAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1486
QY 1517 GAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1576
DB 1486 AAAATGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1545
QY 1577 AAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1636
DB 1546 AAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1605
QY 1637 GAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1696
DB 1606 GAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1656
QY 1697 AAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1756
DB 1657 AAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1716
QY 1757 GAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1816
DB 1717 GAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1776
QY 1817 GAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1876

DB 1777 ATCCATGATGAGAGATTTCCCAACACCTGTTTGAAGAACTTGATCTTTGGAAATGG 1836
QY 1877 CTGGCCGCAAGCCTTGAGAGAGCTGGACCTGGGCGCCGCAAGCCGCTACCCCTGACT 1936
DB 1837 AATGCCACCA-----TCTTCTTAATAGCAAAATGACATTTTGCATCATGGAG 1884
QY 1937 ATCCCCGGGTGGCCCGGACACAGAGAGGCACTATGTGTGGAAGTGCAGACCGGCC 1996
DB 1885 CTTAAGCAATGATCTCTTCAGGACCAAGAGAGATGTGTGTGTGTGTGTGTGTGTGTGTGT 1944
QY 1997 AGCCATGACAGCACTGCGCACAAAGATGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2056
DB 1945 ACCAAGAAAGCAATTTGGGT 2004
QY 2057 CTACCCGCAATCTTACCGACCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2116
DB 2005 ATCCAGGAATCTGGAATGACACCAAGATGATGATGATGATGATGATGATGATGATGATG 2064
QY 2117 TTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2176
DB 2065 ACAGCATCTGGCAATCCCTCTCCAGAGATCATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2124
QY 2177 GAAAGTGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2236
DB 2125 GAAGACTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2184
QY 2237 GAGGAGGATGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2296
DB 2185 AAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2244
QY 2297 TCCGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2356
DB 2245 GAGGCAATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2304
QY 2357 GTCGATACGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2416
DB 2305 GTAGGAGGAGGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2364
QY 2417 ATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2476
DB 2365 GTTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2424
QY 2477 GGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2536
DB 2425 GATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2484
QY 2537 TTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2596
DB 2485 TTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2544
QY 2597 GTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2656
DB 2545 ATTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2604
QY 2657 ATGCTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2716
DB 2605 ATGCTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2664
QY 2717 CTGATTCAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2776
DB 2665 CTGATTCAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2724
QY 2777 CAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2836
DB 2725 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2784
QY 2837 CAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2896
DB 2785 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2844
QY 2897 TTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2956

Db 2845 AAGAGCTACGTTGAGAGCAATCCCTGTGATCTTGAAAGGGCCCTTGACAGCATCCACCT 2904
 QY 2957 GTCCCTTGGCCCGGTTTCTGAAAGCGAGGGGAGAGCGGGCTTCTCCAGACAA 3016
 Db 2905 AGCCAGAGCTCAGCCAGCTGTGGATTGTGAGAGAAATCCCTCATGTATGAGACAA 2964
 QY 3017 GAAG-----CTGAGGACCTGTGCTTGTAGGCTTGTACCATGAGATCTTGTCTGTAC 3070
 Db 2965 GAGGAAGCTCTGAGAGATCTGTATTAAGGATCTCTGACCTTGACATCTCATCTGTAC 3024
 QY 3071 AGCTTCAGCTGAGAGATGAGATGAGATCTCTGAGCTTCCCAAGTGCATCCAGAGAC 3130
 Db 3025 AGCTTCAGCTGAGAGATGAGATGAGATCTCTGAGCTTCCCAAGTGCATCCAGAGAC 3084
 QY 3131 GTGCTGTCTGAGAGATGAGATGAGATCTCTGAGCTTCCCAAGTGCATCCAGAGAC 3190
 Db 3085 CTGGCGGACAGAAATATCTCTGTGAGAGAAAGAGTGAATCTGTGTGCTTGGC 3144
 QY 3191 CTGGCGGAGATCTGAG 3250
 Db 3145 TTGGCCCGGAGATTTTAAAGATCCAGATATGTGTAAGAGAGAGAGAGAGAGAG 3204
 QY 3251 CTGAGATGATGAG 3310
 Db 3205 TTGAAATGATGAG 3264
 QY 3311 TGGTCTTGGAG 3370
 Db 3265 TGGTCTTGGAG 3324
 QY 3371 GTGAGATGAG 3430
 Db 3325 GTAAAGATGATGAG 3384
 QY 3431 GAGCTGCTGAG 3490
 Db 3385 GATATGATGAG 3444
 QY 3491 GCGAGAGCTGAG 3550
 Db 3445 GAG 3504
 QY 3551 CTGAG 3567
 Db 3505 CAG 3521

RESULT 10
 US-09-970-088-9
 : Sequence 9, Application US/09970088
 : Patent No. US20020151489A1
 : GENERAL INFORMATION:
 : APPLICANT: GRAVEREAUX, EDWIN C.
 : APPLICANT: SILVER, MARCY
 : APPLICANT: ISNER, JEFFREY M.
 : APPLICANT: YOUNG, YOUNG-SUP
 : TITLE OF INVENTION: USE OF LYMPHANGIOGENIC AGENTS TO TREAT LYMPHATIC
 : FILE REFERENCE: 71417/55062
 : CURRENT APPLICATION NUMBER: US/09/970,088
 : PRIOR FILING DATE: 2001-10-02
 : NUMBER OF SEQ ID NOS: 14
 : SOFTWARE: PatentIn Ver. 2.1
 : SEQ ID NO 9
 : LENGTH: 420
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 : US-09-970-088-9

Query Match 10.2% Score 420; DB 10; Length 420;
 Host local Similarity 100.0%; Pred. No. 4e-96;

Matches 420; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2111 CAGTCTGTGGTGGCGGAG 2170
 Db 1 CAGTCTGTGGTGGCGGAG 60
 QY 2171 CTGAG 2230
 Db 61 CTGAG 120
 QY 2231 GTGCGGAG 2290
 Db 121 GTGCGGAG 180
 QY 2291 AACTCTCCGCGAG 2350
 Db 181 AACTCTCCGCGAG 240
 QY 2351 ATCTGTGTGGTGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2410
 Db 241 ATCTGTGTGGTGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
 QY 2411 TGTACATGAG 2470
 Db 301 TGTACATGAG 360
 QY 2471 GAGCCCGGGAG 2530
 Db 361 GAGCCCGGGAG 420

RESULT 11
 US-09-970-088-7
 : Sequence 7, Application US/09970088
 : Patent No. US20020151489A1
 : GENERAL INFORMATION:
 : APPLICANT: GRAVEREAUX, EDWIN C.
 : APPLICANT: SILVER, MARCY
 : APPLICANT: ISNER, JEFFREY M.
 : APPLICANT: YOUNG, YOUNG-SUP
 : TITLE OF INVENTION: USE OF LYMPHANGIOGENIC AGENTS TO TREAT LYMPHATIC
 : FILE REFERENCE: 71417/55062
 : CURRENT APPLICATION NUMBER: US/09/970,088
 : PRIOR FILING DATE: 2001-10-02
 : NUMBER OF SEQ ID NOS: 14
 : SOFTWARE: PatentIn Ver. 2.1
 : SEQ ID NO 7
 : LENGTH: 420
 : TYPE: DNA
 : ORGANISM: Oryctolagus cuniculus
 : US-09-970-088-7

Query Match 8.7% Score 356; DB 10; Length 420;
 Best local Similarity 90.5%; Pred. No. 4.9e-80;
 Matches 380; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 2111 CAGTCTGTGGTGGCGGAG 2170
 Db 1 CAGTCTGTGGTGGCGGAG 60
 QY 2171 CTGAG 2230
 Db 61 CTGAG 120
 QY 2231 GTGCGGAG 2290
 Db 121 GTGCGGAG 180
 QY 2291 AACTCTCCGCGAG 2350
 Db 181 AACTCTCCGCGAG 240

D6 181 AACATCTTCCTCCGACGCGTACGTATGTGGAGAGGCCCGCAAGATAGAGCGACATGAGATCGTG 240

QY 2351 ATCTGTGTCGGTACCGGAGGTATGCTGTCTCTTCTGGGTCCTGCTGCTGATATCTTC 241

D6 241 ATCTCGTGTGGACCGCGGCTATTCGCGTGTCTTTTGGGTCCTGCTGCTGATATCTTC 300

QY 2411 TGTAACTGAGAGGCGCGGCCCATCCGACATATCAAGAGCGGCTACCTGTGCTCATCATG 2477

D6 301 TGTAACTGAGAGGCGCGGCCCATCCGAGGACATCAAGAGCGGCTACTGTGCATCATCATG 360

QY 2471 GACCGCGGAGAGGTGTGCTCTGAGAGAGCAATCGATATCTGTCTACGATGCGACGCG 2533

D6 361 GATTCGCGGAGAGTACCTCTCTGAGAGAGCAATGTGAATACCTGTCTACGACGCGACGCA 420

RESULT 12
 US-09-970-088-8
 : Sequence 8, Application US/09970088
 : Patent No. US2002015149A1
 : GENERAL INFORMATION:
 : APPLICANT: GRAVEREAGX, EDWIN C.
 : APPLICANT: SILVER, MARCY
 : APPLICANT: ISNER, JEFFREY M.
 : APPLICANT: YOON, YOUNG-SUP
 : TITLE OF INVENTION: USE OF LYMPHANGIOGENIC AGENTS TO TREAT LYMPHATIC
 : TITLE OF INVENTION: DISORDERS
 : FILE REFERENCE: 7117/55062
 : CURRENT APPLICATION NUMBER: US/09/970,698
 : CURRENT FILING DATE: 2001-10-02
 : PRIOR APPLICATION NUMBER: 65/237,171
 : PRIOR FILING DATE: 2000-10-02
 : NUMBER OF SEQ ID NOS: 14
 : SOFTWARE: PatentIn Ver. 2.1
 : SEQ ID NO. 8
 : LENGTH: 420
 : TYPE: DNA
 : ORGANISM: Bos sp.
 : US-09-970-088-8

US-09-970-088-10
Sequence 10, Application US/09970088
Patent No. US2002015489A1
GENERAL INFORMATION:
APPLICANT: GRAVEREAUX, EDWIN C.
APPLICANT: SILVER, MARCY
APPLICANT: ISNER, JEFFREY M.
APPLICANT: YOON, YOUNG-SUP
TITLE OF INVENTION: USE OF LYMPHANGIOGENIC AGENTS TO TREAT LYMPHATIC
DISEASES
FILE REFERENCE: 71417/55062
CURRENT APPLICATION NUMBER: US/09/970,088
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/237,171
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENGTH: 420
TYPE: DNA
ORGANISM: Mus sp.
US-09-970-088-10

RESULT 14
 US-09-944-807-9
 : Sequence 9, Application US/09944807
 : Patent No. US20020119494A1
 : GENERAL INFORMATION:
 : APPLICANT: Boehringer Ingelheim Pharma KG
 : TITLE OF INVENTION: Method for identifying substances which positively
 : influence inflammatory conditions of chronic
 : TITLE OF INVENTION: inflammatory airway diseases
 : FILE REFERENCE: 082_00n
 : CURRENT APPLICATION NUMBER: US/09/944_807
 : CURRENT FILING DATE: 2001-08-31
 : PRIOR APPLICATION NUMBER: UK 00211484.1
 : PRIOR FILING DATE: 2000-09-01
 : NUMBER OF SEQ. ID NOS: 24
 : SOFTWARE: PatentIn Ver. 2.1
 : SEQ. ID NO 9

[illegible]

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? ANTI-SENSE: NO
? FRAGMENT TYPE: N-terminal
? FEATURE:
? NAME/KEY: mat_peptide
? LOCATION: 113-2006

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QY	1081	GCCTCTAAGCTGGCAGCGTACACCCCGCCCGCAATTCAGTGTACAGAGATGGAAAGCC	11404
Db	1081	GCCTCTAAGCTGGCAGCGTACACCCCGCCCGCAATTCAGTGTACAGAGATGGAAAGCC	11404
QY	1141	ACTGTCCGGGGCCACAGTGCACATGGCTTGGTCTCAAGAGGTACACAGAGCCAGCAC	12004
Db	1141	ACTGTCCGGGGCCACAGTGCACATGGCTTGGTCTCAAGAGGTACACAGAGCCAGCAC	12004
QY	1201	AGGCACCTTACACCCCTGACCTGTGGAACTTCGCTGCTAGGCTGAGACGACATCAGCTC	12604
Db	1201	AGGCACCTTACACCCCTGACCTGTGGAACTTCGCTGCTAGGCTGAGACGACATCAGCTC	12604
QY	1261	GGAGTGGTGGTAAATGTATGTCCCGCCCGCCAGATACATAGAAAGAGGCTCTCCCGCACAT	13204
Db	1261	GGAGTGGTGGTAAATGTATGTCCCGCCCGCCAGATACATAGAAAGAGGCTCTCCCGCACAT	13204
QY	1321	CTACTCGCGTACAGCCCGCAGGCGCTCTACCTGACACGGAGCTACGGGGGTGCCCTGCGTCT	13804
Db	1321	CTACTCGCGTACAGCCCGCAGGCGCTCTACCTGACACGGAGCTACGGGGGTGCCCTGCGTCT	13804
QY	1381	CAGCATCCAGTGGCACTGGGGGGCCCTGGAGACCCCTGCAAAATGTTTGCCACAGGTAGTCT	14404
Db	1381	CAGCATCCAGTGGCACTGGGGGGCCCTGGAGACCCCTGCAAAATGTTTGCCACAGGTAGTCT	14404
QY	1441	CCGGCGCGCGCAGCAGCAGACCTCATGCGCACAGTGCCTGATGTGAGAGAGGGGTGCACAC	15004
Db	1441	CCGGCGCGCGCAGCAGCAGACCTCATGCGCACAGTGCCTGATGTGAGAGAGGGGTGCACAC	15004
QY	1501	GCAGGATGCGGTACACCCCATCCAGACATCCGACACCTGGACCCGAGCTTTGTGGAGCAAA	15604
Db	1501	GCAGGATGCGGTACACCCCATCCAGACATCCGACACCTGGACCCGAGCTTTGTGGAGCAAA	15604
QY	1561	GAAATACAGCTGAGCAAGCTGGTGGATCCAGAAATCCCAAGCTGTGCGCATGTACAAAGTG	16204
Db	1561	GAAATACAGCTGAGCAAGCTGGTGGATCCAGAAATCCCAAGCTGTGCGCATGTACAAAGTG	16204
QY	1621	TGTGCTCTCCACACAGGTGGCCAGAGTAGCGGCTATCTACTTATATGTACACCAT	16804
Db	1621	TGTGCTCTCCACACAGGTGGCCAGAGTAGCGGCTATCTACTTATATGTACACCAT	16804
QY	1681	CCCGACGCGGCTTACCATATCGAATCGCAAGCATCCGACGAGCTACTAGAGGGCCAGCCGAT	17404
Db	1681	CCCGACGCGGCTTACCATATCGAATCGCAAGCATCCGACGAGCTACTAGAGGGCCAGCCGAT	17404
QY	1741	GCTCTCTAGCTGGCAAGCCGACAGCTACTACAGTAAAGATCTGTGCGTATGACGCTCAAA	18004
Db	1741	GCTCTCTAGCTGGCAAGCCGACAGCTACTACAGTAAAGATCTGTGCGTATGACGCTCAAA	18004
QY	1801	CCTGTGCAGCTGTACATATGAGATGGCAATGGACCCGTTCTGTCTGTGATCCAAAGATGTGA	18604
Db	1801	CCTGTGCAGCTGTACATATGAGATGGCAATGGACCCGTTCTGTCTGTGATCCAAAGATGTGA	18604
QY	1861	TCGTGTCGACACCCCTCTGGCGCGTCAAGCCTGTGAGTAGGTGCAACTGTGGGTCGCGCACGC	19204
Db	1861	TCGTGTCGACACCCCTCTGGCGCGTCAAGCCTGTGAGTAGGTGCAACTGTGGGTCGCGCACGC	19204
QY	1921	CACGCTAGCCTGTAGTATCTCCCGCGCTGCTGGCGCCGACAGCAGAGGGCTACATATGTGTGGA	19804
Db	1921	CACGCTAGCCTGTAGTATCTCCCGCGCTGCTGGCGCCGACAGCAGAGGGCTACATATGTGTGGA	19804
QY	1981	AATGCAAGACCGGCGACGACATATGACAGCATGTGCACAAAGTACCTGTGCTGCGAGGC	20404
Db	1981	AATGCAAGACCGGCGACGACATATGACAGCATGTGCACAAAGTACCTGTGCTGCGAGGC	20404
QY	2041	CCTGGAAGCCCTCGGCTACCCAGAACTTGAACCTCTGTGTAACGTGAGCGACTTC	21004
Db	2041	CCTGGAAGCCCTCGGCTACCCAGAACTTGAACCTCTGTGTAACGTGAGCGACTTC	21004
QY	2101	GCTGGAATATCATGATCTTTGGTGTGCTGGACCGAGCCGCCACAGTATGTGTGTACAAAGA	21604
Db	2101	GCTGGAATATCATGATCTTTGGTGTGCTGGACCGAGCCGCCACAGTATGTGTGTACAAAGA	21604

D	3241	CGCGTGGCCGCTCAAGTGGATAGGAGCCCTGAAGGATCTTGAGCAAGGTGACACCGAGA	3300
Q	3301	GAGTGACGTGTGTCTCTTGGAGTGTCTCTTGAGAGATCTCTCTGAGAGGCTCTCC	3360
D	3301	GAGTGACGTGTGTCTCTTGGAGTGTCTCTTGAGAGATCTCTCTGAGAGGCTCTCC	3360
Q	3361	GTACCGCTGGGTGCAGATCAATGAGAGTCTGGCCAGCGGCTGAGACAGGCAAGAAGT	3420
D	3361	GTACCGCTGGGTGCAGATCAATGAGAGTCTGGCCAGCGGCTGAGACAGGCAAGAAGT	3420
Q	3421	GAGGCGCCCGAGACTGGCCATCTCCGCTTACGACGCGATATGCTGACTCTGGGTGAG	3480
D	3421	GAGGCGCCCGAGACTGGCCATCTCCGCGCTATGAGCGCGATATGCTGACTCTGGGTGAG	3480
Q	3541	GGGCGAGGGGCTCCGAAAGAGAGAGAGGTCTGCATGGCCCGCGGCACTCTCGAGCTC	3600
D	3541	GGGCGAGGGGCTCCGAAAGAGAGAGAGGTCTGCATGGCCCGCGGCACTCTCGAGCTC	3600
Q	3601	AGAAAGAGGCTAGCTTCTCGTAGGTCTCCACCATGGGCTTACACATGGCCGAGGTACGC	3660
D	3601	AGAAAGAGGCTAGCTTCTCGTAGGTCTCCACCATGGGCTTACACATGGCCGAGGTACGC	3660
Q	3661	TGAGGACAGCGCCCGCCAAAGCTGTGAGGGCCACAGGCTGGCGGCGAGTATACAACTGGT	3720
D	3661	TGAGGACAGCGCCCGCCAAAGCTGTGAGGGCCACAGGCTGGCGGCGAGTATACAACTGGT	3720
Q	3721	GTCCTTCCCGGGTGCCTGGGCGAGAGGGCTGAGACCGGTGGTCTCCAGATGAGAGC	3780
D	3721	GTCCTTCCCGGGTGCCTGGGCGAGAGGGCTGAGACCGGTGGTCTCCAGATGAGAGC	3780
Q	3781	ATTGAGGAATTCCTCCATGACCTTACCACTTACAAAGCTCTGTGGACAACTGATAGA	3840
D	3781	ATTGAGGAATTCCTCCATGACCTTACCACTTACAAAGCTCTGTGTGACAACTGATAGA	3840
Q	3841	CAGTGGGATGTCTGGCTCGAGACGTTTACAGATGAGATGAGACAGCTATGACAGAGA	3900
D	3841	CAGTGGGATGTCTGGCTCGAGACGTTTACAGATGAGATGAGACAGCTATGACAGAGA	3900
Q	3901	AAGCGGCTTACGCTGTAAAGAGCTGGCCAGATGTGGCTGTACACAGGCAACCTTGA	3960
D	3901	AAGCGGCTTACGCTGTAAAGAGCTGGCCAGATGTGGCTGTACACAGGCAACCTTGA	3960
Q	3961	CTCCCAAGAGGCGGGGCGGCTGTAGGGGGGGGCGGAGAGGCGAGGTTTACAGA	4020
D	3961	CTCCCAAGAGGCGGGGCGGCTGTAGGGGGGGGCGGAGAGGCGAGGTTTACAGA	4020
Q	4021	CAGCGAGTATGGGAGCTGTGGAGCCCAAGCGAGAGAGACCACTGCTCCCGTGTGCCG	4080
D	4021	CAGCGAGTATGGGAGCTGTGGAGCGCAAGCGAGAGAGACCACTGCTCCCGTGTGCCG	4080
Q	4081	CGTCACTTCTTACAGCAACAGCACTACTAA 4111	
D	4081	CGTCACTTCTTACAGCAACAGCACTACTAA 4111	
RESULT 2			
US-08-901-710-3			
Sequence 3, Application US/08901710			
Patent No. 6107046			
GENERAL INFORMATION:			
APPLICANT: Alltalo, Kari			
APPLICANT: Appelkova, Olga			
APPLICANT: Pajusola, Katri			
APPLICANT: Armstrong, Elna			
APPLICANT: Korhonen, Jaana			
APPLICANT: Kaipainen, Aija			
APPLICANT: Mälikäinen, Maria-Terttu			
TITLE OF INVENTION: P174, A RECEPTOR TYROSINE KINASE, AND USES			
TITLE OF INVENTION: THEROOF			

QY	361	GTATCATTAAGGGACGACATCCAGGGGACACAGGGCGGCACTCTCAAGCTGTGTGTAAGA	420
Db	361	GTATCATTAAGGGACGACATCCAGGGGACACAGGGCGGCACTCTCAAGCTGTGTGTAAGA	420
QY	421	CTTTGAGCAGCCATTTCATCAACAAAGCTGTACAGCTCTTTGGTCAACAGAAAGAGCCAT	480
Db	421	CTTTGAGCAGCCATTTCATCAACAAAGCTGTACAGCTCTTTGGTCAACAGAAAGAGCCAT	480
QY	481	GTGGGTGCTCCTGTCTGGGTGTTCATCCCCGGGCTTAATGTCAACCTGGGGCTCCGAAAGTTC	540
Db	481	GTGGGTGCTCCTGTCTGGGTGTTCATCCCCGGGCTTAATGTCAACCTGGGGCTCCGAAAGTTC	540
QY	541	GGTGTCTGTGGCCAGACGGGGAGAGAGGTGTGTGGGAATGACCGGGCGGGCATGTCTGTCTC	600
Db	541	GGTGTCTGTGGCCAGACGGGGAGAGAGGTGTGTGGGAATGACCGGGCGGGCATGTCTGTCTC	600
QY	601	CAGCGTACTGTGTGCACAGTGGCTTGTACCTGTACGTGTGAGATCACTGTGGAGAGCTAGGA	660
Db	601	CAGCGTACTGTGTGCACAGTGGCTTGTACCTGTACGTGTGAGATCACTGTGGAGAGCTAGGA	660
QY	661	CTTCCTTCCAAACCCCTCCCTGGGTGTACATATACAGCAAGCAAGCTATATACATCCAGCT	720
Db	661	CTTCCTTCCAAACCCCTCCCTGGGTGTACATATACAGCAAGCAAGCTATATACATCCAGCT	720
QY	721	GTTCGCCAGGAGAGTGGCTGTGAGAGCTGTGTGTAGGGGAAGAACTGTGTCTGAATGTCAACGT	780
Db	721	GTTCGCCAGGAGAGTGGCTGTGAGAGCTGTGTGTAGGGGAAGAACTGTGTCTGAATGTCAACGT	780
QY	781	GTGGGCTGTAGTTTAACTAGGTGTCAAGCTTTGTACTGTGAACTACCCAGGAAAGTAGGAGA	840
Db	781	GTGGGCTGTAGTTTAACTAGGTGTCAAGCTTTGTACTGTGAACTACCCAGGAAAGTAGGAGA	840
QY	841	GGGGGGTAACTGGGTGGCCGAGAGGAGAGCTCCGACAGCAACCCACAGAACTGTCCAGAT	900
Db	841	GGGGGGTAACTGGGTGGCCGAGAGGAGAGCTCCGACAGCAACCCACAGAACTGTCCAGAT	900
QY	901	CCTGACCATCCAAACGCTACAGCCAGCAAGCAAGCAAGCTGGGTGTGTGTGCAAGGCCAACAA	960
Db	901	CCTGACCATCCAAACGCTACAGCCAGCAAGCAAGCAAGCTGGGTGTGTGTGCAAGGCCAACAA	960
QY	961	GGGCACTCCAGCGATTTTGGGGAGAACACGAGATCATATGTGTGATGAAAATCCCTTTATCAG	1020
Db	961	GGGCACTCCAGCGATTTTGGGGAGAACACGAGATCATATGTGTGATGAAAATCCCTTTATCAG	1020
QY	1021	CGTTCACATGGCTTAAAGAACCCATCTGTGAGGACCAAGGAGAGCAAGCTGTGTGAAGCT	1080
Db	1021	CGTTCACATGGCTTAAAGAACCCATCTGTGAGGACCAAGGAGAGCAAGCTGTGTGAAGCT	1080
QY	1081	GGCCCTGAAAGCTGTGAGAGCTAACCCTCTGGCCAGTTCCAGTGTACAAAGATGGAAGAGC	1140
Db	1081	GGCCCTGAAAGCTGTGAGAGCTAACCCTCTGGCCAGTTCCAGTGTACAAAGATGGAAGAGC	1140
QY	1141	ACTGTCCGGGGGCGACATATCCACATGCTCTGTGTGTAAAGAGGTGACAGAGGCGACAGC	1200
Db	1141	ACTGTCCGGGGGCGACATATCCACATGCTCTGTGTGTAAAGAGGTGACAGAGGCGACAGC	1200
QY	1201	AGGCACTCAACCTCTGGCCCTGTGTGAAGTCCGCTCTGTGGCTTGAGGCGCAACATCAGCT	1260
Db	1201	AGGCACTCAACCTCTGGCCCTGTGTGAAGTCCGCTCTGTGGCTTGAGGCGCAACATCAGCT	1260
QY	1261	GGAGCTGTGTGATGTGTGCCCCCCCCAGATAGATATGAAAGAGAGCTCTCTCCCTCCAGCAT	1320
Db	1261	GGAGCTGTGTGATGTGTGCCCCCCCCAGATAGATATGAAAGAGAGCTCTCTCCCTCCAGCAT	1320
QY	1321	CTATCTCGGTTCACAGGCTGTCAAGGCTCTCAATGTGCACAGGCTATAGGGGTGGCCCTGGCTCT	1380
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QY	1381	CAGCACTCAGAGAGGCACTAGGAGGCTCTGTGAGACCTGTGAAAGATTTTGGCCAGGCTATGCT	1440
Db	1381	CAGCACTCAGAGAGGCACTAGGAGGCTCTGTGAGACCTGTGAAAGATTTTGGCCAGGCTATGCT	1440


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QY 901 CTTGACATTCACAGGTACAGGACGACCTGAGGCTCTATGCTGTGAAGGCCAACAA 960
DB 901 CTTGACATTCACAGGTACAGGACGACCTGAGGCTCTATGCTGTGAAGGCCAACAA 960
QY 961 CCGCATTCACAGGTATTCGAGGAGAGCAGGAGGTCATGTTGATGAAAATCCCTTATAG 1020
DB 961 CCGCATTCACAGGTATTCGAGGAGAGCAGGAGGTCATGTTGATGAAAATCCCTTATAG 1020
QY 1021 CTTGACATTCACAGGTATTCGAGGAGAGCAGGAGGTCATGTTGATGAAAATCCCTTATAG 1080
DB 1021 CTTGACATTCACAGGTATTCGAGGAGAGCAGGAGGTCATGTTGATGAAAATCCCTTATAG 1080
QY 1081 GCGCGTGAAGCTGAGGAGGTCATGTTGATGAAAATCCCTTATAG 1140
DB 1081 GCGCGTGAAGCTGAGGAGGTCATGTTGATGAAAATCCCTTATAG 1140
QY 1141 ACTGTCGAGGAGGTCATGTTGATGAAAATCCCTTATAG 1200
DB 1141 ACTGTCGAGGAGGTCATGTTGATGAAAATCCCTTATAG 1200
QY 1201 AGGCACTACAGGTCATGTTGATGAAAATCCCTTATAG 1260
DB 1201 AGGCACTACAGGTCATGTTGATGAAAATCCCTTATAG 1260
QY 1261 GAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
DB 1261 GAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
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DB 1321 CTTGACATTCACAGGTATTCGAGGAGAGCAGGAGGTCATGTTGATGAAAATCCCTTATAG 1380
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DB 1381 CAGCATTCACAGGTATTCGAGGAGAGCAGGAGGTCATGTTGATGAAAATCCCTTATAG 1440
QY 1441 CCGGAGGTCATGTTGATGAAAATCCCTTATAG 1500
DB 1441 CCGGAGGTCATGTTGATGAAAATCCCTTATAG 1500
QY 1501 CTTGACATTCACAGGTATTCGAGGAGAGCAGGAGGTCATGTTGATGAAAATCCCTTATAG 1560
DB 1501 CTTGACATTCACAGGTATTCGAGGAGAGCAGGAGGTCATGTTGATGAAAATCCCTTATAG 1560
QY 1561 GAGATTCACAGGTATTCGAGGAGAGCAGGAGGTCATGTTGATGAAAATCCCTTATAG 1620
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QY 1681 GAGATTCACAGGTATTCGAGGAGAGCAGGAGGTCATGTTGATGAAAATCCCTTATAG 1740
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QY 1981 GAGATTCACAGGTATTCGAGGAGAGCAGGAGGTCATGTTGATGAAAATCCCTTATAG 2040
DB 1981 GAGATTCACAGGTATTCGAGGAGAGCAGGAGGTCATGTTGATGAAAATCCCTTATAG 2040
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[illegible]

2521 TGCAGCTAGTGGCAATTCCTCCGAGAGAGGCTCCACCTCGGAGATGCTTGGCTACGG 2580
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 2642 GAGCTGCGAGAGAGTGGTGGAGAGCTCGGCTTTCGCTACAGAGGCGACAGAGTGTGA 2640
 2701 GTGAGAGCTGCAAGATTCCTACATTCGCAAGAGTGTGAAGTGTGAAGTGTGAAGTGTGA 2760
 2702 GTGAGAGCTGCAAGATTCCTACATTCGCAAGAGTGTGAAGTGTGAAGTGTGAAGTGTGA 2760
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 2761 GAGCTGCGAGAGAGTGGTGGAGAGCTCGGCTTTCGCTACAGAGGCGACAGAGTGTGA 2820
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 2882 GAGCTGCGAGAGAGTGGTGGAGAGCTCGGCTTTCGCTACAGAGGCGACAGAGTGTGA 2940
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 2942 GAGCTGCGAGAGAGTGGTGGAGAGCTCGGCTTTCGCTACAGAGGCGACAGAGTGTGA 3000
 3001 GAGCTGCGAGAGAGTGGTGGAGAGCTCGGCTTTCGCTACAGAGGCGACAGAGTGTGA 3060
 3002 GAGCTGCGAGAGAGTGGTGGAGAGCTCGGCTTTCGCTACAGAGGCGACAGAGTGTGA 3060
 3061 GAGCTGCGAGAGAGTGGTGGAGAGCTCGGCTTTCGCTACAGAGGCGACAGAGTGTGA 3120
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 3182 GAGCTGCGAGAGAGTGGTGGAGAGCTCGGCTTTCGCTACAGAGGCGACAGAGTGTGA 3240
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 3242 GAGCTGCGAGAGAGTGGTGGAGAGCTCGGCTTTCGCTACAGAGGCGACAGAGTGTGA 3300
 3301 GAGCTGCGAGAGAGTGGTGGAGAGCTCGGCTTTCGCTACAGAGGCGACAGAGTGTGA 3360
 3302 GAGCTGCGAGAGAGTGGTGGAGAGCTCGGCTTTCGCTACAGAGGCGACAGAGTGTGA 3360
 3361 GAGCTGCGAGAGAGTGGTGGAGAGCTCGGCTTTCGCTACAGAGGCGACAGAGTGTGA 3420
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 3481 GAGCTGCGAGAGAGTGGTGGAGAGCTCGGCTTTCGCTACAGAGGCGACAGAGTGTGA 3540
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 3542 GAGCTGCGAGAGAGTGGTGGAGAGCTCGGCTTTCGCTACAGAGGCGACAGAGTGTGA 3600
 3601 GAGCTGCGAGAGAGTGGTGGAGAGCTCGGCTTTCGCTACAGAGGCGACAGAGTGTGA 3660

3601 AGAAGAGGCGACCTTCCTGCAAGTGTTCACACATGAGCTCTACACATCCGCGAGCTGAGCG 3660
 3661 TGAGAGAGCG 3720
 3662 TGAGAGAGCG 3720
 3721 GTCCTTTCGCGAGAGTGGTGGAGAGCTCGGCTTTCGCTACAGAGGCGACAGAGTGTGA 3780
 3722 GTCCTTTCGCGAGAGTGGTGGAGAGCTCGGCTTTCGCTACAGAGGCGACAGAGTGTGA 3780
 3781 ATTGAGAGATTCCTCCATGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3840
 3782 ATTGAGAGATTCCTCCATGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3840
 3841 CAGTGGAGTGGTGGAGAGCTCGGCTTTCGCTACAGAGGCGACAGAGTGTGAAGTGTGA 3900
 3842 CAGTGGAGTGGTGGAGAGCTCGGCTTTCGCTACAGAGGCGACAGAGTGTGAAGTGTGA 3900
 3901 AAGCGCTTCAGCT 3914
 3902 AAGCGCTTCAGCT 3914

RESULT 5
 US-08-795-430-1
 Sequence 1, Application US/08795430
 Patent No. 6130071
 GENERAL INFORMATION:
 APPLICANT: Altaleo, Kari
 TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
 TITLE OF INVENTION: Protein and Gene, Mutants Thereof, and Uses Thereof
 NUMBER OF SEQUENCES: 57
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: United States of America
 ZIP: 60606-6402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/795,430
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/EP196/00427
 FILING DATE: 01-AUG-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE: 06/671,573
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE: 28-JUN-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/501,132
 FILING DATE: 14-FEB-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE: 06/585,895
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/510,133
 FILING DATE: 01-AUG-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/340,011
 FILING DATE: 14-NOV-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Gass, David A.
 REGISTRATION NUMBER: 38,153
 REFERENCE/DOCKET NUMBER: 28967/33691
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/474-6300

QY 1 CCAGCCGAGAGGAGCCGAAATGATAGAGGAGGAGAGCCGCTGTGGCTGCAAGATGAGGCTGTG 60
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D	901	CCTGACCATCCAAAGCTCAGACACGACGACGACCTGGGTGTATGTGTCAAGGCCAACAA	960
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D	1201	AGGACCTACACCTCGCGCTGTGGAGATCTCGTGGCTGGCGTGAAGGGCAAACTACGCT	1260
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Q	1381	CAGATTCGATGGCAGTGTGGGGCCCTGGACACCTCTGACAGATGTTGCCACGGTATGCT	1440
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D	1681	CCCCGACGGCTACCATCGAATCCAAACCATCCGAGGAGCTACTAGAGGGCCAGCGGT	1740
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Db	3361	GTACCCCTGGGGTGCAGATCAATGAGAGATTGTGCGACGGCTGAAGACGGCCACAGAT	3420
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QY	3661	TGAGGACAGCCCGCGCAAGCTTCAGCAGCAGCTGGCGCGCGCAAGATTACACTGGGT	3720
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RESULT 6

US-09-355-700-1

Sequence 1, Application US/09355700

Patent No. 6361946

GENERAL INFORMATION:

APPLICANT: Ludwig Institute for Cancer Research

Helinski University Licensing

Altairo, Karliu S. only

Joukov, Vladimir (U.S. only)

TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)

Protein and Gene, Mutants Thereof, and Uses Thereof

NUMBER OF SEQUENCES: 59

```

1  ADDRESS/SEQUENCE ADDRESS:
2  ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Horun
3  STREET: 6300 Sears Tower, 233 South Wacker Drive
4  CITY: Chicago
5  STATE: Illinois
6  COUNTRY: United States of America
7  ZIP: 60606-6402
8
9  COMPUTER READABLE FORM:
10 MEDIUM TYPE: Floppy disk
11 COMPUTER: IBM PC compatible
12 OPERATING SYSTEM: PC-DOS/MS-DOS
13 SOFTWARE: Patent: Release #1.0, Version #1.30
14
15 CURRENT APPLICATION DATA:
16 APPLICATION NUMBER: US/09/355,700
17 FILING DATE: 05-NOV-1994
18 CLASSIFICATION: <Unknown>
19
20 PRIOR APPLICATION DATA:
21 APPLICATION NUMBER: 08/795,430
22 FILING DATE: 05-FEB-1997
23 APPLICATION NUMBER: PCI/F196/00427
24 FILING DATE: 01-AUG-1996
25 APPLICATION NUMBER: 08/671,573
26 FILING DATE: 28-JUN-1996
27 APPLICATION NUMBER: 08/501,132
28 FILING DATE: 14-FEB-1996
29 APPLICATION NUMBER: 08/585,895
30 FILING DATE: 12-JAN-1996
31 APPLICATION NUMBER: 08/510,133
32 FILING DATE: 01-AUG-1995
33 APPLICATION NUMBER: 08/340,011
34 FILING DATE: 14-NOV-1994
35
36 ATTORNEY/AGENT INFORMATION:
37 NAME: Gass, David A.
38 REGISTRATION NUMBER: 38,153
39 REFERENCE/DOCKET NUMBER: 28967/34140
40
41 TELECOMMUNICATION INFORMATION:
42 TELEPHONE: 312/474-6300
43 TELEFAX: 312/474-0448
44
45 INFORMATION FOR SEQ ID NO: 1:
46
47 SEQUENCE CHARACTERISTICS:
48 LENGTH: 4416 base pairs
49 TYPE: nucleic acid
50 STRANDNESS: single
51 TOPLOGY: linear
52 FEATURE TYPE: CDS
53
54 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
55
56 us-09-355-700-1:
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58 Query Match 95.2% Score 3912.4 DB 4 Length 4416:
59 Best Local Similarity 100.0% Pctd. No. 0:
60 Matches 3913: Conservative 0: Mismatches 1: Indels 0: Gaps 0:

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Dh	3421	GAGGGCGCGGAGCTTGGCCACTCCGCGTAAACCGGATGATCATCTGATCTGTCGG	3480
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Dh	3481	AACCTTCGAGGCGACACTGTATCTTCGAGAGTGTGATGATCTTCGGGGAGCTGCTCA	3540
QY	3541	GGGCGAGGCGCTTCGCAAGAGAGAGAGGCTGCGATGGCGCGCGGAGCTTCGAGAGCTC	3600
Dh	3541	GGGCGAGGCGCTTCGCAAGAGAGAGAGGCTGCGATGGCGCGGAGCTTCGAGAGCTC	3600
QY	3601	AGAGAGAGGCTAGCTTCTTCGAGAGTGTTCAGAGCTGAGCTTCAATGGCGGCGGAGGCTGAGC	3660
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QY	3661	TAGAGAGAGGCGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCT	3720
Dh	3661	TAGAGAGAGGCGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCT	3720
QY	3721	GGCGCTTCGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCT	3780
Dh	3721	GGCGCTTCGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCT	3780
QY	3781	ATTGAGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCT	3840
Dh	3781	ATTGAGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCT	3840
QY	3841	CAGTGGCTGAGTGTGCTGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCT	3900
Dh	3841	CAGTGGCTGAGTGTGCTGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCT	3900
QY	3901	AAGCGAGTTCAGCT 39.4	
Dh	3901	AAGCGAGTTCAGCT 39.4	
RESULT B			
US-DB-222.616-32			
Sequence 31, Application US/8222616			
Patient No. 5955177			
GENERAL INFORMATION:			
APPLICANT: Bennett, Brian D.			
APPLICANT: Goodale, David			
APPLICANT: Lee, James M.			
APPLICANT: Matthews, William			
APPLICANT: Tsai, Siao Ping			
TITLE OF INVENTION: PROTEIN TYROSINE KINASE ASOINISI			
TITLE OF INVENTION: ANTIBODIES			
NUMBER OF SEQUENCES: 42			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: Genentech, Inc.			
STREET: 460 Point San Bruno Blvd			
CITY: South San Francisco			
STATE: California			
COUNTRY: USA			
ZIP: 94080			
COMPUTER READABLE FORM:			
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk			
COMPILER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: patis (genentech)			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/08/222.616			

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1      : FILING DATE: 4-APR-1994
2      : CLASSIFICATION: 530
3      : PRIOR APPLICATION DATA:
4      : APPLICATION NUMBER: PCT/US93/00586
5      : FILING DATE: 22-JAN-1993
6      : PRIOR APPLICATION DATA:
7      : APPLICATION NUMBER: 07/826935
8      : FILING DATE: 22-JAN-1992
9      : ATTORNEY/AGENT INFORMATION:
10     : NAME: Lee, Wendy M.
11     : REGISTRATION NUMBER:
12     : REFERENCE/DOCKET NUMBER: 821P2
13     : TELECOMMUNICATION INFORMATION:
14     : TELEPHONE: 415/225-1994
15     : TELEFAX: 415/952-9881
16     : TELEX: 910/371-7168
17     : INFORMATION FOR SEQ ID NO: 31:
18     : SEQUENCE CHARACTERISTICS:
19     : LENGTH: 4425 bases
20     : TYPE: nucleic acid
21     : STRANDEDNESS: single
22     : TOPOLOGY: linear
23     :
24     : US-08-222-616-31
25
26     Query Match          95.28: Score 3912.4; DB 1; Length 4425;
27     Best Local Similarity 100.0%; Pred. No. 0;
28     Matches 3913; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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32     QY 61 CCGAGGACCTCTCGACACGGCTGTGTGAGTGGTACTCATGACCCCGCCGACTTGAACAT 120
33     DB 72 CCGTGGGACCTCTGACACGGCTGTGTGAGTGGTACTCATGACCCCGCCGACTTGAACAT 131
34     QY 121 CACGAGGAGTGCACACGTCTGACACCGCGGTGACACGCTGTGCATCTCTCTGACGGGACA 180
35     DB 132 CACGAGGAGTGCACACGTCTGACACCGCGGTGACACGCTGTGCATCTCTCTGACGGGACA 191
36     QY 181 GCACGCCCTCCGAGTGGGCTTGGCCAGGAGACTGAGAGGCGCCACGCCACGGGAGACAMGA 240
37     DB 192 GCACGCCCTCCGAGTGGGCTTGGCCAGGAGACTGAGAGGCGCCACGCCACGGGAGACAMGA 251
38     QY 241 CACGCGAGACACAGGCGGTGGTGGGAGACTGCGAGGGGACACAGACGCCGCGCTACTGGCAA 300
39     DB 252 CACGCGAGACACAGGCGGTGGTGGGAGACTGCGAGGGGACACAGACGCCGCGCTACTGGCAA 311
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41     DB 312 GGTGTGTGTGTTGACAGAGGATATATGTCATACGACACAGAGGAGTGTACGTGTGCTACTACAA 371
42     QY 361 GTACATCAAGGACGACATCGAGGGGACACAGGCGCCCGACGCTCTACTGCTGTGTGAGACA 420
43     DB 372 GTACATCAAGGACGACATCGAGGGGACACAGGCGCCCGACGCTCTACTGCTGTGTGAGACA 431
44     QY 421 CTTTGCAGCGCATTCATCAACAAAGCCTTACACGCTTGTGGTCAACAGGAAGACAGCCCAT 480
45     DB 432 CTTTGCAGCGCATTCATCAACAAAGCCTTACACGCTTGTGGTCAACAGGAAGACAGCCCAT 491
46     QY 481 GTGGGTGCCCTGTGTGTGTGTCATCCCGCGGCTCATATGTACGCTGTGCGCTCGCAAAAGTC 540
47     DB 492 GTGGGTGCCCTGTGTGTGTGTCATCCCGCGGCTCATATGTACGCTGTGCGCTCGCAAAAGTC 551
48     QY 541 GGTGCTGTGGCCAGACGGGACAGAGGTGTGTGTGATGTACCGGCGGGGGCATGCTGTGTTC 600
49     DB 552 GGTGCTGTGGCCAGACGGGACAGAGGTGTGTGTGATGTACCGGCGGGGGCATGCTGTGTTC 611
50     QY 601 CACGGCCACTGTCACACATGCTCTGTACTGTGACGTGGACACCAAGCTGGGGGAGACACAGA 660
51     DB 612 CACGGCCACTGTCACACATGCTCTGTACTGTGACGTGGGGAGACCAAGCTGGGGGAGACACAGA 671
52     QY 661 CTTCCTCTTCCAAACCGCTCTCTGTGGTGCATTCACAGGACACAGAGCTCTATGACATCCAGCT 720

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 Db 732 GTTCCCCAGGAGTTCGTGTGACCTCTGTGAGGCAACAGCTGCTGTGAATTCAGCT 792
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DB 1992 AGTGAAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2051
QY 2041 CCGTGAAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 2100
DB 2052 CCGTGAAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 2111
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RESULT 10
 PCT-US95-04228-31
 ? Sequence 31, Application PCT/US9504228
 ? GENERAL INFORMATION:
 ? APPLICANT: Genentech, Inc.
 ? APPLICANT: Bennett, Brian D.
 ? APPLICANT: Goeddel, David
 ? APPLICANT: Lee, James M.
 ? APPLICANT: Matthews, William
 ? APPLICANT: Tsai, Shao Ping
 ? APPLICANT: Wood, William I.
 ? TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
 ? NUMBER OF SEQUENCES: 45
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: Genentech, Inc.
 ? STREET: 460 Point San Bruno Blvd
 ? CITY: South San Francisco
 ? STATE: California
 ? COUNTRY: USA
 ? ZIP: 94080
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: 5.25 Inch, 360 Kb floppy disk
 ? COMPUTER: IBM PC compatible
 ? OPERATING SYSTEM: PC-DOS/MS-DOS
 ? SOFTWARE: patin (Genentech)
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: PCT/US95/04228
 ? FILING DATE:
 ? CLASSIFICATION:
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: 08/222616
 ? FILING DATE: 04-Apr-1994
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Wendy M. Lee
 ? REGISTRATION NUMBER: 00,000
 ? REFERENCE/DOCKET NUMBER: 821P3PCT
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: 415/225-1994
 ? TELEFAX: 415/952-9881
 ? TELEX: 910/371-7168
 ? INFORMATION FOR SEQ ID NO: 31:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 4425 bases
 ? TYPE: nucleic acid
 ? STRANDEDNESS: single
 ? TOPOLOGY: linear

PCT-US95-04228-31

Query Match 95.2% Score 3912.4 DB 5; Length 4425;
Best Local Similarity 100.0%; Pref. No. 0;
Matches 3913; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACGCCGACGCGCGGAGATGACAGCGGCGCGCGCTGCTGCGACAGTGGCTCTG 60
DB 12 CCACGCCGACGCGCGGAGATGACAGCGGCGCGCGCTGCTGCGACAGTGGCTCTG 71
QY 61 CTTGGGACCTCTGACGCGCTGCTGAGTGGCTATGCTCAAGCCGCGGACCTGGAACAT 120
DB 72 CTTGGGACCTCTGAGAGCGCTGCTGAGTGGCTATGCTCAAGCCGCGGACCTGGAACAT 131
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RESULT 11
 US-08-446-648-45
 : Sequence 45, Application US/08446648
 : Patent No. 6331302
 : GENERAL INFORMATION:
 : APPLICANT: Genentech, Inc.
 : APPLICANT: Bennett, Brian D.
 : APPLICANT: Goeddel, David
 : APPLICANT: Lee, James M.
 : APPLICANT: Matthews, William
 : APPLICANT: Tsai, Siao Ping
 : APPLICANT: Wood, William I.
 : TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
 : NUMBER OF SEQUENCES: 45
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Genentech, Inc.
 : STREET: 460 Point San Bruno Blvd
 : CITY: South San Francisco
 : STATE: California
 : COUNTRY: USA
 : ZIP: 94080

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Db 4424 AGAGCCCAAGAGAGAGCTTCTGAGAGAGCAATGCAATTACTTCTCTACGA 4483

APPLICANT: Lee, James M.
APPLICANT: Matthews, William
APPLICANT: Tsai, Siao Ping
APPLICANT: Wood, William T.
TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: pedit (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04228

FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/222616

FILING DATE: 04-APR-1994

ATTORNEY/AGENT INFORMATION:
NAME: Wendy M. Lee

REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 821P3PCT

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225 1994

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 6827 bases

TYPE: nucleic acid

STRANDNESS: single

TOPOLOGY: linear

PCT-US95-04228-17

Query Match 25.3% Score 1040.2 DB 5 Length 6827

Best Local Similarity 98.3% Pred. No. 4.6e-202

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DB 2647 ATTCCTGTGAG 2588
QY 3206 TACAAAG 3265
DB 2587 TACAAAG 2528

QY 3266 CCTGAAAGCATCTTCGAG 3325
DB 2527 CCTGAAAGCATCTTCGAG 2468
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DB 2407 GAGTCTGCGAGGCTGAG 2348
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DB 2227 GAGTCTGCTGAG 2168
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DB 1987 ACGACCTCAAG 1928
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ORIGIN
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Best Local Similarity 99.38; Pred. No. 3.3e-76;
Matches 481; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

QY 3461 ATCTGAACTGCTGTCGGAGACCCAAAGGCAAGCTGATTCGAGCTGGAG 3526
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QY 3641 GAGAGCGCGAGCTGTCGAGAGGCAAGCTGTCGAGCTGGAGCTGGAG 3700
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LOCUS BB647382
DEFINITION BB647382 RIKEN full-length enriched, 10 days neonate cerebellum Mus
ACCESSION BB647382
VERSION BB647382.1 GI:16481711
KEYWORDS EST.
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
1 (bases 1 to 570)
REFERENCE
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
Hirotsu,K., Horii,F., Ishii,Y., Ito,M., Kawai,J., Kono,H., Konda,
M., Koyama,S., Matsuyama,T., Miyazaki,A., Momota,K., Ono,M.,
Okazaki,Y., Okado,T., Saito,K., Sakai,C., Sakai,K., Sano,H., Sasaki,
D., Shibata,K., Shinagawa,A., Shitaki,I., Sogabe,Y., Suzuki,H.,
Tagami,M., Tadawa,A., Takahashi,F., Takeda,Y., Tanaka,I., Toyu,T.,
Muramatsu,M. and Hayashizaki,Y.

TITLE
JOURNAL
COMMENT
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
Contact: Yoshitake Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,
M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
Wagl,K., Fujiwara,S., Inoue,K., Togawa,Y., Iwata,M., Ohara,E.,
Matsubara,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsunaga,
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and
Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multichannel sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Kono,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,
Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamane,I., Alizawa,
K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
Hayashizaki,Y.
Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
e mouse tissues.

FEATURES
Source
Location/Qualifiers
1..570
/organism="Mus musculus"
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prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGATTCGAGAGCTTTTCTTTTCTTTTCTTTT 3']. cDNA was
prepared by using triazole thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to R1 - 10.0 and subtraction to R1 - 100.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GAGAGAGATTCGAGAGCTTTTCTTTTCTTTTCTTTT 3'].
cDNA was cloned into the XhoI and BamHI sites.
Vector: a modified plasmid pUC19 after bulk excision
from Lambda phage. Cloning sites, 5' end: Salt; 3' end:
BamHI".

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Best Local Similarity 84.4%; Pred. No. 4.1e-76;
Matches 481; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

KEYWORDS EST.
SOURCE COW.
ORGANISM Bos taurus
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
COMMENT
TITLE
JOURNAL
MEDLINE
COMMENT
FEATURES
SOURCE
BASE COUNT
ORIGIN
Query Match.
Best Local Similarity 84.4%
Matches 378: Conservative 0: Mismatches 70: Indels 0: Gaps 0:

EST.
COW.
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 448)
Smith, T. P., D., Grosse, W. M., Freking, H. A., Roberts, A. J., Stone, R. T.,
Casas, F., Wray, J. E., White, J., Cho, C., Fahnenkrug, S. C., Bennett,
G. B., Heaton, M. P., Laegreid, W. M., Rohrer, G. A., Chitko, M. K., C. G.,
Peters, G., Holt, L., Karaycheva, S., Chang, F., Quackenbush, J., and
Keeler, J. W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-640 (2001)
2118013
Contact: Smith TPI,
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smitht@mail.mars.usda.gov
Single pass sequencing. Bases called and alt-trimmed with phred
v6.98094.e. Vector identified by cross-match with the -minscore 18
and mismatch 12 options.
PCR primers:
FORWARD: AGGAAGACCTATGACCA
BACKWARD: GTTCCCATGACGACG
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Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendinosus muscle, and fetal
longissimus muscle."
104 a 134 c 131 g 78 t 1 others

Query Match.
Best Local Similarity 84.4%
Matches 378: Conservative 0: Mismatches 70: Indels 0: Gaps 0:

EST.
COW.
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 448)
Smith, T. P., D., Grosse, W. M., Freking, H. A., Roberts, A. J., Stone, R. T.,
Casas, F., Wray, J. E., White, J., Cho, C., Fahnenkrug, S. C., Bennett,
G. B., Heaton, M. P., Laegreid, W. M., Rohrer, G. A., Chitko, M. K., C. G.,
Peters, G., Holt, L., Karaycheva, S., Chang, F., Quackenbush, J., and
Keeler, J. W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-640 (2001)
2118013
Contact: Smith TPI,
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smitht@mail.mars.usda.gov
Single pass sequencing. Bases called and alt-trimmed with phred
v6.98094.e. Vector identified by cross-match with the -minscore 18
and mismatch 12 options.
PCR primers:
FORWARD: AGGAAGACCTATGACCA
BACKWARD: GTTCCCATGACGACG
Plates: 130 row: 0 column: 20
Seq primer: ATTAGGTCACATTATG
Location/Qualifiers
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Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendinosus muscle, and fetal
longissimus muscle."
104 a 134 c 131 g 78 t 1 others

DB 361 TCACAGGCTTTACGGGCAAGGCGGCGGCGGCGGCTCCAGTCACGAAGCA 420
QY 3024 AGACCTGTGCTGAGCCGCTGACCAT 3051
DB 421 AGACCTGTGCTGAGCCGCTGACCAT 448
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DEFINITION
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TCBAPID6345 pediatric pre-B cell acute lymphoblastic leukemia
Baylor-HSC project-TCBAP6345, mRNA
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Accession
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
SOURCE
BASE COUNT
ORIGIN
Query Match.
Best Local Similarity 97.4%
Matches 339: Conservative 0: Mismatches 9: Indels 0: Gaps 0:

EST.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 348)
Wei, Y., Tsang, Y. T. M., Mei, G., Ku, J. M., Ali-Osman, J. R., F. R., Muzny, D.,
Bouck, J., Gibbs, R. A., and Margolin, J. F.
Pediatric Leukemia cDNA Sequencing Project
Unpublished (2000)
Contact: Dr. Judith F. Margolin
Texas Children's Cancer Center and Human Genome Sequencing Center
1102 Bates, MC3-3320 Houston, TX 77030, USA
Tel: 832-824-4536
Fax: 832-825-4038
Email: clones@ccc.org
Citation: Carninci, P. and Hayashizaki, Y. High efficiency
full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
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Location/Qualifiers
1..348
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First strand cDNA was primed with an anchored
XhoI-oligo(dT) primer (5'-GGAGAGCTGAGGCGGCGGAGGAG(T)VN
3'-V-A-C-G; N-A-C-G-T) and then dg tailed. Second strand
was primed with a BamHI-dC primer (5'-AGAGAGCTGAGGCGGCGGAGGAG(T)VN
3'-V-A-C-G; N-A-C-G-T) and then dg tailed. Second strand
Double-stranded cDNA was then digested with BamHI and XhoI
and directionally cloned into the BamHI and SalI sites of
lambda pSB vector. Library was constructed by Wei Yu at RIKEN
of Japan (Carninci P., Westover A., Nishiyama Y., Ohsumi T.,
Itoh M., Nagaoaka S., Sasaki, N., Okazaki Y., Muramatsu M.,
Schneider C., Hayashizaki Y., High efficiency selection of
full-length cDNA by improved biotinylated cap trapper,
DNA Res 4: 1, 61-6, Feb 28, 1997).
74 a 105 c 107 g 60 t 2 others

Query Match.
Best Local Similarity 97.4%
Matches 339: Conservative 0: Mismatches 9: Indels 0: Gaps 0:

EST.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 348)
Wei, Y., Tsang, Y. T. M., Mei, G., Ku, J. M., Ali-Osman, J. R., F. R., Muzny, D.,
Bouck, J., Gibbs, R. A., and Margolin, J. F.
Pediatric Leukemia cDNA Sequencing Project
Unpublished (2000)
Contact: Dr. Judith F. Margolin
Texas Children's Cancer Center and Human Genome Sequencing Center
1102 Bates, MC3-3320 Houston, TX 77030, USA
Tel: 832-824-4536
Fax: 832-825-4038
Email: clones@ccc.org
Citation: Carninci, P. and Hayashizaki, Y. High efficiency
full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Seq primer: M13 primer.
Location/Qualifiers
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/organism="Homo sapiens"
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First strand cDNA was primed with an anchored
XhoI-oligo(dT) primer (5'-GGAGAGCTGAGGCGGCGGAGGAG(T)VN
3'-V-A-C-G; N-A-C-G-T) and then dg tailed. Second strand
was primed with a BamHI-dC primer (5'-AGAGAGCTGAGGCGGCGGAGGAG(T)VN
3'-V-A-C-G; N-A-C-G-T) and then dg tailed. Second strand
Double-stranded cDNA was then digested with BamHI and XhoI
and directionally cloned into the BamHI and SalI sites of
lambda pSB vector. Library was constructed by Wei Yu at RIKEN
of Japan (Carninci P., Westover A., Nishiyama Y., Ohsumi T.,
Itoh M., Nagaoaka S., Sasaki, N., Okazaki Y., Muramatsu M.,
Schneider C., Hayashizaki Y., High efficiency selection of
full-length cDNA by improved biotinylated cap trapper,
DNA Res 4: 1, 61-6, Feb 28, 1997).
74 a 105 c 107 g 60 t 2 others

BASE COUNT	225 a	195 c	232 g	183 t
CRIGIN				

LOCUS DEFINITION				
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Mt-P-CPI.nzb-m-17-0-U1.s1	Mt-P-CPI	Sus scrofa	cDNA clone	
ACCESSION	B0604389			
VERSION	B0604389.1	GI:21511115		
KEYWORDS	EST.			
SOURCE	pig.			
ORGANISM	Sus scrofa			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.			
TITLE	1 (bases 1 to 697)			
	Honaldi,M.F., Lennon,G. and Soares,J.B.			
	Normalization and subtraction: two approaches to facilitate gene			

REFERENCE	1 (bases 1 to 697)
AUTHORS	Ronaldo, M.F., Lennon, G. and Soares, M.B.
TITLE	Normalization and subtraction: two approaches to facilitate
JOURNAL	discovery
MEDLINE	genome Res. 6 (9), 791-806 (1996)
COMMENT	97044477
	Contact: Tugale CK

Molecular Genetics Laboratory, Department of Animal Science
Iowa State University
201 Kildee Hall, Ames, IA 50011-3150, USA
Tel: 5152944252
Fax: 5152944201

Fax: 319.279.2401
 Email: cktugle@iastate.edu
 Tissue Procurement: Dr. Chris Tugle, Iowa State University
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 FORWARD

FEATURES	Location/Qualifiers
source	1. 697
	/organism="Sus scrofa"
	/strain="Growth"

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/note="Vector: pRT3D-Pac (Pharmacia) with a modified polylinker. Site_1: Not I; Site_2: EcoRI. The M1-P-CPI library is normalized library derived from the M1-P-Cf0 library, ultimately derived from uterus tissue. For a

detailed description of the library from which this clone was derived, please visit our web site at <http://pigsty.genome.iasstate.edu/>. The procedure used to create this library has been previously described (Bonaldo Lennon and Soares. Genome Research 6: 791-905, 1995).

BASE COUNT	139 a	181 c	181 g	196 t
TAG_SEQ-AGTCGATCG*				
TAG_TISSUE-uterus				
TAG_LIB-M1-p-CPI				

Query Match	6.98	Score 284.6	DB 14	Length 697
Best Local Similarity	65.68	Pred. NO.	3.4e-47	
Matches 4320	Coverage 100%	Unaligned 327		

Index	Conservative	Mismatches	Indels	Gaps
2213	AGCTGAGCATCCAGAGGCGCTGCGGAGAGATGCGGAGCGCTATCTGTGACGCGTGC	2272		
695	AGCGCTGTTTATGAAAGACTCACGAGAAAGATGAAGAGCGGTATACATCATGACCCCTAC	636		

[illegible]

QY 233 GGCACATGAGATCCGATCCTCTTCGGACCGGCGCATCGCTCTCTTCGGTC 2392
 :||| ||||| | | ||| ||||| | | | | ||||| ||
 Db 575 TCCACCTCGAGCTGATCACCTGACGTACTGTGTGGCGCACACCTCTTTCGGTC 516

515 CTGCTACCCCTCTCTTATTCGGAAGAACTGAAGAGGCTCTC---CTCTGCTCTTAAAGCTGAC 450
 2393 CTTCTCTCTCTCTCACTCTCTGTGATCATGAGGAGGCCGCGCCACGACAGATCATAGACACGGC 2452

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Db 458 TACCTGTCATATATCATGAGACCCAGAGAGAGTCCCTTGATGAGCAGTGGCAAGGCTG 399
QY 2513 TCTTACGATGCCAGCCAGTGGGAATTCCCCGAGAGGGCTGACCTGGGAGAGTGTCTG 2572
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Db 398 CTTTACGATGCCAGAGTGGAGTTGGCCGGAGAGACTGAGCTGGGTAATCACTG 339
QY 2573 GGCACGGGGCTTGGGAGAGTGGTGAAGCTCTGGCTTTCGGCATCCAGAGGGCAGC 2632
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 338 GGAAGAGGGGCTTTTGGAAAGTGGTCCAGGGCATCTGCCCTTGGTATTAGAAATCACC 279
QY 2633 AGCTGTGACAGCGTGGCGGTGAATGCTTAAAGAGAGAGGGGACGAGCAGCAGC 2692
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Db 278 AGCTGGCGGAGCGGTACCTGTAAAAATCTGAAAAAGAGGGGCCACCGCCAGCGAGTACAAA 219
QY 2693 GCGGTATCTGAGAGCTCAAGATCTCATTACATGCGGCAACACACTCAAGGTGTGCAAG 2752
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QY 2753 CTCCCTGGGGGCTGACAGCAAGCCGCAAGGGGCCCTCATGCTGATGCTGGAGTTCTGCAAG 2812
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Search completed: May 1, 2003, 10:56:35
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ried. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	4111	100.0	4111	21	AA062405	Human Flt4/VEGFR-3
2	4111	100.0	4795	21	AA037816	Human Flt4 receptor
3	4111	100.0	4795	21	AA055334	Human tyrosine kinase
4	4209.4	100.0	4111	22	AA068952	Human Flt4/VEGFR-3
5	3912.4	95.2	4195	21	AA037815	Human Flt4 receptor
6	3912.4	95.2	4195	21	AA055333	Human tyrosine kinase
7	3912.4	95.2	4425	16	AA003090	Protein tyrosine kinase
8	3912.4	95.2	4108	16	AA003104	Plasminogen activator
9	3910.8	95.1	4195	17	AA012068	Flt4 receptor tyrosine kinase

10	3888.6	94.6	3897	24	ABL91573	Human polynucleotide
11	3826	93.1	4450	21	AA622130	Nucleotide sequence
12	1040.2	25.3	6827	14	AA049753	ptk gene SAL-S1.
13	1040.2	25.3	6827	16	AAAT03101	Protein tyrosine-k
14	713	17.3	5404	17	AA387835	Murine foetal liver k
15	713	17.3	5404	20	AAAT7516	Murine flk-1 cDNA
16	713	17.3	5406	13	AA029557	flk-1 cDNA sequence
17	713	17.3	5406	14	AA053504	Murine flk-1 cDNA
18	713	17.3	5406	14	AA035251	Murine flk-1 cDNA
19	713	17.3	5406	14	AA040916	Human flk-1 coding
20	713	17.3	5406	16	AA081014	Murine flk-1 cDNA
21	713	17.3	5406	16	AA079070	Flk1 receptor proto
22	713	17.3	5406	18	AAAT72119	Mouse flk-1 cDNA.
23	709.8	17.3	5470	15	AA064449	Murine flk-1 recep
24	683	16.6	4044	24	ABL91751	Sequence of murine
25	683	16.6	4071	20	AAV98829	Human polynucleoti
26	683	16.6	4071	24	ABL91754	Human receptor tyro
27	683	16.6	4225	25	AAAT83308	Human polynucleoti
28	681.4	16.6	4071	13	AA028372	Human VEGFR-2 enc
29	681.4	16.6	4236	19	AAV34763	A novel type III f
30	543.2	13.2	4017	24	ABL91752	Human KDR genomic
31	541.6	13.2	7680	23	AA570286	Human polynucleoti
32	285.4	7.2	1444	22	AAA91075	DNA encoding novel
33	281.8	6.9	3992	23	AA579665	Flt1 receptor fusi
34	281.8	6.9	3992	23	ABK48105	DNA encoding novel
35	266.4	6.5	6390	24	AA579665	Human macrophage
36	266.4	6.5	6390	23	AA584936	DNA encoding novel
37	256.6	6.2	2555	18	AAAT95837	DNA for VEGF recep
38	242.8	5.9	3453	14	AA053502	Murine flk-2 cDNA.
39	242.8	5.9	3453	14	AA035249	Murine flk-2 coding
40	242.8	5.9	3453	14	AA040914	Murine flk-2 cDNA.
41	242.8	5.9	3453	16	AA081012	Flk2 receptor proto
42	242.8	5.9	3453	16	AA079068	Mouse flk-2 cDNA.
43	242.8	5.9	3453	17	AAAT8713	Human foetal liver
44	242.8	5.9	3453	18	AAAT72118	Murine flk-2 recep
45	242.8	5.9	3453	20	AAAT7514	Murine flk-2 cDNA

ALIGNMENTS

RESULT 1	
AAC62405	
ID	AAC62405 standard. cDNA: 4111 bp.
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AC	AAC62405:
XX	
DT	31-JAN-2001 (first entry)
XX	
DE	Human FLT4/VEGFR-3 coding sequence.
XX	
KM	Human: FLT4: fms-like tyrosine kinase 4; lymphoedema;
KM	vascular endothelial growth factor receptor 3; VEGFR-3;
KM	Milroy-Notre syndrome; lymphoedema praecox; ss.
XX	
OS	Homo sapiens.
XX	
PN	W0200058511-A1.
XX	
PD	05-OCT-2000.
XX	
PF	26-MAR-1999. 99WO-US06133.
XX	
PR	26-MAR-1999. 99WO-US06133.
XX	
PA	(LUDW-) LUDWIG INST CANCER RES.
PA	(UTHE-) UNIT HELSINKI LICENSING LTD OY.
PA	(UVP1-) UNIV PITTSBURGH.
XX	
PI	Ferrell RE, Allitalo K, Finegold DN, Karkkainen M;
XX	
DR	WPI: 2000-679298/66.
DR	P-PSDB: AAB29047.

XX Screening a human subject for increased risk of developing a lymphatic
 PT disorder, comprises assaying a nucleic acid to determine a mutation
 PT altering the sequence of a vascular endothelial growth factor
 PT receptor-3 -

PS Claim 14: Page 46-52: 76pp. English.

XX The present sequence is the coding sequence for the human vascular
 CC endothelial growth factor receptor 3 (VEGFR-3, also known as Flt4 or
 CC fms-like tyrosine kinase 4). It was used in the methods of the invention,
 CC which involve the screening of individuals to determine which VEGFR-3
 CC alleles they possess and thus their likelihood of developing hereditary
 CC lymphoedema. Conditions associated with lymphoedema include Milroy's
 CC syndrome, which is early onset lymphoedema and lymphoedema praecox, which
 CC is late onset.

XX Sequence 4111 BP: 846 A: 1273 C: 1298 G: 694 T: 0 other:

Query Match 100.0% Score 4111: DB 21: Length 4111:

Best Local Similarity 100.0%: Pctd. No. 0: Mismatches 0: Indels 0: Gaps 0:

Matches 4111: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

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 QY 6: CCTGGAGCTGTGAGAGGCTGTGAGTGGTACTCATATGACCCCGGACCTTGAAACAT 120
 DB 61 CTTGGAGCTGTGAGAGGCTGTGAGTGGTACTCATATGACCCCGGACCTTGAAACAT 120
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 QY 181 GCACCTCTGTGAGAGGCTTGGCCAGGAGCTCAGAGCCCGCCAGCCAGGACAGCAAGA 240
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 DB 241 CAGGAGAGAGAGGAGGAGTGTGTCAGAGCTGCGAGGGGACAGAGCGCCCTTACTGCA 300
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 DB 301 GGTGTTGCTGCTGACAGAGTACATGCAAGGACAGCAAGCCACTTACTGCTACTGCA 360
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QY	3421	GAGGGCCCGGAGCGTGGCCATCTCGCGCATAGCGCGCATCATGCTGAACTGCTGGCG	3480
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QY	3781	ATTGAGGAATTCCTCCATGACCTTCAAGAGATCTCAAAAGGCTCTGTGACAAACGACGAGA	3840
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QY	3961	CTTCCCAAGGAGAGCGCGCGGCGGCTGAAATGGGGGCGCCGAAGAGGCTAGGTGTTTACAA	4020
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QY	4021	CAGCGAGTATGCGAGCTGTGTGAGGCAAGCGCAGAGAGACCATTCCTCCCGCTGTGGCGG	4080

|||||
 4321 CACCGACTAAGGACCTCTCGACCCAGGAGAGAGACCACTCTCCCGTGTCCCG 4080
 4081 CGTCACTTCTTCAGACACAGCTACTAA 4111
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 4081 CGTCACTTCTTCAGACACAGCTACTAA 4111

RESULT 2
 AAA37816
 ID AAA37816 standard; cDNA: 4795 BP.
 AAA37816;
 15-ZAN-2602 (first entry)

Human FLT4 receptor tyrosine kinase long form coding sequence.
 Human FLT4 receptor tyrosine kinase; antibody: extracellular domain;
 lymphatic vessel detection; lymphatic tissue; lymph node tissue;
 endothelial venule; diagnosis; lymphoma; long form; ss.

Homo sapiens.
 Key Location/Qualifiers
 CDS 22..4111
 /tag: a
 /product: FLT4 receptor tyrosine kinase long form

US6107040-A. 1
 22-AUG-2000.
 28-JUN-1997; 9705-050710.
 09-DEC-1992; 9205-095951.
 09-JUN-1994; 9405-025754.
 14-NOV-1994; 9405-0340011.

(CRIN) CRON CORP.
 (LUDW-) LUDWIG INST CANCER RES.
 Alizadeh K, Aprelikova O, Armstrong E, Kornblum J, Kalpalan A;
 Matkalin M, Rajusola K;
 MPI: 2000-5/1323/53.
 P ENR: AAY90366.

Antibody to extracellular domain of or to an epitope unique to a
 vertebrate FLT4 receptor tyrosine kinase protein; useful for diagnosing
 lymphoma and imaging lymphatic vessels or high endothelial venules in
 tissue.

Disclosure: Column: 55-66; 66pp; English.

This sequence encodes the human FLT4 receptor tyrosine kinase long
 form protein. The invention relates to an antibody (I) specific to the
 extracellular domain of or to an epitope unique to a vertebrate FLT4
 receptor tyrosine kinase protein (II). A composition comprising (I) is
 useful for detecting lymphatic vessels, lymphatic tissue comprising lymph
 node tissue or high endothelial venules in an organism preferably mammal
 especially human. The method comprises administering the composition and
 detecting (I) bound to lymphatic vessels, lymphatic tissue or high
 endothelial venules. (I) is also useful for screening a biological sample
 for the presence of (II) or diagnosing a disease state. The diagnosing
 method of the disease state preferably lymphoma comprises obtaining a
 tissue sample on a vertebrate organism suspected of being in a diseased
 state characterized by in FLT4 expression in lymphatic cells or high
 endothelial venules and screening the diseased state utilizing (I).
 (I) is also useful for imaging lymphatic vessels or high endothelial
 venules in a tissue by contacting the tissue with (I) and imaging the
 vessels by detecting (I) bound to the tissues.

SQ Sequence 4795 BP; 977 A; 1490 C; 1494 G; 834 T; 0 other;
 Query Match 100.0%; Score 4111; DB 21; Length 4795;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 4111; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

1 CCACGGCAGCGGGGAGATGTCACCGGGGCGCGCGCTGTGCTGACATGTGGACTCTG 60
 1 CCACGGCAGCGGGGAGATGTCACCGGGGCGCGCGCTGTGCTGACATGTGGACTCTG 60
 61 CCGGGAGCTCTGAGAGCGGCTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 120
 61 CCGGGAGCTCTGAGAGCGGCTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 120
 121 CACGAGAGAGTCAACATGATGACACCGGTGTGAGAGCTGTGCTGCTGCTGCTGCT 180
 121 CACGAGAGAGTCAACATGATGACACCGGTGTGAGAGCTGTGCTGCTGCTGCTGCT 180
 181 GCACCCCTGAGTGGGCTTGGCTGAGAGCTCAAGAGGCGCCAGCCCGGACCAAGCA 240
 181 GCACCCCTGAGTGGGCTTGGCTGAGAGCTCAAGAGGCGCCAGCCCGGACCAAGCA 240
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 901 CCGACCATCCCAAGGTAGCCAGACGACCTGGCTGTGTGTGTGTGTGTGTGTGTGT 960
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 961 CCGATCCAGCATTTCGAGAGAGACAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020

[illegible]

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QY	2161	GCAGAGCGCTCTGGAGGAAAAAGTGTGGAGTCGACTTGGCCGANTTCACACAGAAAGTTGAG	2220
Db	2161	GCAGAGCGCTCTGGAGGAAAAAGTGTGGAGTCGACTTGGCCGANTTCACACAGAAAGTTGAG	2220
QY	2221	CATCCAGCGGTGCGAGGAGGAGATGATGGAGCGATATCTGTGACGTGTCCAAAGACGAA	2280
Db	2221	CATCCAGCGGTGCGAGGAGGAGATGATGGAGCGATATCTGTGACGTGTCCAAAGACGAA	2280
QY	2281	GGCGTCGGCTCACTCCCTCCGACCCGTGGCTGTGGAAAGCGCCGAGAGATTAAGGCGACAT	2340
Db	2281	GGCGTCGGCTCACTCCCTCCGACCCGTGGCTGTGGAAAGCGCCGAGAGATTAAGGCGACAT	2340
QY	2341	GGAGATGGTATCTTGTGTGCGTACCGGCGTCATGGCTGTCTTTCTTGGGTCTCTCTCT	2400
Db	2341	GGAGATGGTATCTTGTGTGCGTACCGGCGTCATGGCTGTCTTTCTTGGGTCTCTCTCT	2400
QY	2401	CCTCATCTCTGTACACATGAGAGAGCCCGGCTACGCGACATCAAGAGCGGCTACCTGTG	2460
Db	2401	CCTCATCTCTGTACACATGAGAGAGCCCGGCTACGCGACATCAAGAGCGGCTACCTGTG	2460
QY	2461	CATCATCATGACCCCGGAGGACCTCCCTCTGGAGAGCAATGGCAATACCTGTGCTTACGA	2520
Db	2461	CATCATCATGACCCCGGAGGAGCTCCCTCTGGAGAGCAATGGCAATACCTGTGCTTACGA	2520
QY	2521	TGCCACGCAATGGGGAATTCGCCGGAAGTGGTGAACCTGGGAGATGCTCGGCTACGG	2580
Db	2521	TGCCACGCAATGGGGAATTCGCCGGAAGTGGTGAACCTGGGAGATGCTCGGCTACGG	2580
QY	2581	CGCCCTCGGGAAGGTGGTGGAGAGCGCTCCCTTGGGATCATCAAGAGGACGACGCTGTGA	2640
Db	2581	CGCCCTCGGGAAGGTGGTGGAGAGCGCTCCCTTGGGATCATCAAGAGGACGACGCTGTGA	2640
QY	2641	CACGCTGGCCCTGAAAAATGCTGAAAGAGGGGACCCGACGCGGAGACCGCGCTGTAT	2700
Db	2641	CACGCTGGCCCTGAAAAATGCTGAAAGAGGGGACCCGACGCGGAGACCGCGCTGTAT	2700
QY	2701	GTCCGACCTAGATTCCTCATTTCAATCGGCACACCTTCAAGTGTGCAACTCTCTCGG	2760
Db	2701	GTCCGACCTAGATTCCTCATTTCAATCGGCACACCTTCAAGTGTGCAACTCTCTCGG	2760
QY	2761	GGCGGTGACCAACGCGGAGGGGCCCTCTGATGGTGTGTTGAGATTCTGCAAGTACGGCAA	2820
Db	2761	GGCGGTGACCAACGCGGAGGGGCCCTCTGATGGTGTGTTGAGATTCTGCAAGTACGGCAA	2820
QY	2821	CGCTCGCAACTCTGTGCGCGCCAAAGGGAGACCCCTTCAAGCCCTCGCCGCGAGAAAGTCTCC	2880
Db	2821	CGCTCGCAACTCTGTGCGCGCCAAAGGGAGACCCCTTCAAGCCCTCGCCGCGAGAAAGTCTCC	2880
QY	2881	CGAGGACGCGCAACGCTTCGCGCGCATGTGTGAGCTTGGCAGGCTGGATCGAGAGCGGCC	2940
Db	2881	CGAGGACGCGCGACGCTTCGCGCGCATGTGTGAGCTTGGCAGGCTGGATCGAGAGCGGCC	2940
QY	2941	GGGAGAGAGGACAGAGGTCCTTTCGCGGGGTGTGCAAGACGAGGGCGGACGAGGCG	3000
Db	2941	GGGAGAGAGGACAGAGGTCCTTTCGCGGGGTGTGCAAGACGAGGGCGGACGAGGCGG	3000
QY	3001	GGCTTCCTCCAGACCAAGAGCTGTGGCTTGAAGCCGCTGACATGAGAACATCT	3060
Db	3001	GGCTTCCTCCAGACCAAGAGCTGTGGCTTGAAGCCGCTGACATGAGAACATCT	3060
QY	3061	TGTCCTGCTACAGCTTCAGGTGGCCAGAGAGGATGGAGTTCCTGGCTTCCCGAAAGTGCA	3120
Db	3061	TGTCCTGCTACAGCTTCAGGTGGCCAGAGAGGATGGAGTTCCTGGCTTCCCGAAAGTGCA	3120
QY	3121	CGACACGACCTGGCTGTGTGCGGAACATGTGTGTCGTGGGAAAAGCAAGTGGTGAAGATCTG	3180
Db	3121	CGACACGACCTGGCTGTGTGCGGAACATGTGTGTCGTGGGAAAAGCAAGTGGTGAAGATCTG	3180
QY	3181	TGACCTTTGGGCTTCGCGGCGACATCTACAAAGACCCGTGACTAGCTGCGCAAGGGCGATGCG	3240

Db	3421	GAAGGCCCCGAGCTGGCCACTCCCGCATACCGCCGCATCATCTGTAACCTCTGTGTCGG	3480
OY	3481	AGACCCCAAGGCGACAGCTGCGATTTCTTGAGAGCTGGTGGAGATCTTGGGGGAGCTTGTCTCA	3540
Db	3481	AGACCCCAAGGCGACAGCTGCGATTTCTTGAGAGCTGGTGGAGATCTTGGGGGAGCTTGTCTCA	3540
OY	3541	GGGCAAGGGCCCTCGAAGAGAGAGAGAGGTCTGCATGGCCCCGGCAGCTTCTACAGCTC	3600
Db	3541	GGGCAAGGGCCCTCGAAGAGAGAGAGAGGTCTGCATGGCCCCGGCAGCTTCTACAGCTC	3600
OY	3601	AGAGAGGAGGAGGTTTCTGCGAGAGTGTCCACCATGGCCCTACACATGGCCCGAGGTCAAGCC	3660
Db	3601	AGAGAGGAGGAGGTTTCTGCGAGAGTGTCCACCATGGCCCTACACATGGCCCGAGGTCAAGCC	3660
OY	3661	TGAGGACACGCCCCCAAGGCTGCGAGGCGCCACAGGCTTGCCCGCAGGATTTACAACTGGGT	3720
Db	3661	TGAGGACACGCCCCCAAGGCTGCGAGGCGCCACAGGCTTGCCCGCAGGATTTACAACTGGGT	3720
OY	3721	GTCTCTTCCCGGGTGGCTGGCCAGAGGGGCTGACACCGGTGGTCTCCAGCATGAGAGC	3780
Db	3721	GTCTCTTCCCGGGTGGCTGGCCAGAGGGGCTGACACCGGTGGTCTCCAGCATGAGAGC	3780
OY	3781	ATTTGAGGAATTCGCCATGACCTCCCAACGACCTACAAAGCTCTGTGAGCAACCGACAGACA	3840
Db	3781	ATTTGAGGAATTCGCCATGACCTCCCAACGACCTACAAAGCTCTGTGAGCAACCGACAGACA	3840
OY	3841	CAGTGGATGCTGCTGGCCTGGAGGAGTTTGAGCAGATGAGAGAGGCAATGACAAAGA	3900
Db	3841	CAGTGGATGCTGCTGGCCTGGAGGAGTTTGAGCAGATGAGAGAGGCAATGACAAAGA	3900
OY	3901	AAGCGGCTTCAGCTGTAAAGAGCTGGCGAGATGTGCTGTGACCAAGGACACACCTGGA	3960
Db	3901	AAGCGGCTTCAGCTGTAAAGAGCTGGCGAGATGTGCTGTGACCAAGGACACACCTGGA	3960
OY	3961	CTCCCAAGGAGGCGCGCGCGGCTGACGCGGGGGGCTCCGAGGAGGCGCAGGTGTTTACAA	4020
Db	3961	CTCCCAAGGAGGCGCGCGCGGCTGACGCGGGGGGCTCCGAGGAGGCGCAGGTGTTTACAA	4020
OY	4021	CAGCAGATGAGGAGAGCTGTGGAGGCTAAGGACAGAGAGACCATGCTCCCGCTGTGCGG	4080
Db	4021	CAGCAGATGAGGAGAGCTGTGGAGGCTAAGGACAGAGAGACCATGCTCCCGCTGTGCGG	4080
OY	4081	CGTGACTTCTTACAGCAACACAGCTACTAA 4111	
Db	4081	CGTGACTTCTTACAGCAACACAGCTACTAA 4111	

RESUL 4
AAC68952

ID AAC68952 standard; cdna: 4111 bp.

XX AC AAC68952;

XX AC

XX DT 27-FEB-2001 (first entry)

XX DE Human FLT4/VEGFR-3 coding sequence.

XX DE

XX KM Human; gene therapy; lymphatic disorder; hereditary lymphoedema; FLT4;

XX KM vascular endothelial growth factor receptor; 3; VEGFR-3; VEGF-C; VEGF-D;

XX KM fms-like tyrosine kinase 4; ss.

XX OS Homo sapiens.

XX OS

XX FT Key Location/Qualifiers

XX FT CDS 20..4111

XX FT /tag= a

XX FT /product= "Human FLT4/VEGFR-3"

XX PN CA2283470.AL

XX PD 26-SEP-2000.

XX PE 29-SEP-1999, 99CA-2283470.

Page 9

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OY	541	GGTGGTGGGCGAGAGGGGCGAGAGAGTGGTGGGGATATGACCGGGGGGATATCTCTGTTC	600
Db	541	GGTGGTGGGCGAGAGGGGCGAGAGAGTGGTGGGGATATGACCGGGGGGATATCTCTGTTC	600
OY	601	CAGCGCATGCTGCAGATGCCCTGTATCTGCAGAGTGGGACGACACTGGGGAGACAGGA	660
Db	601	CAGCGCATGCTGCAGATGCCCTGTATCTGCAGAGTGGGACGACACTGGGGAGACAGGA	660
OY	661	CTTCTCTTCCAAAGCCCTTCTGTGTGCATACAGAGCAAGAGCTATGATATCCAGCT	720
Db	661	CTTCTCTTCCAAAGCCCTTCTGTGTGCATACAGAGCAAGAGCTATGATATCCAGCT	720
OY	721	GTTCGCGAGAGAGTGGCTGAGAGCTGCTGGTAAAGGGAGAAAGTGGTCTTAATGCACCGT	780
Db	721	GTTCGCGAGAGAGTGGCTGAGAGCTGCTGGTAAAGGGAGAAAGTGGTCTTAATGCACCGT	780
OY	781	GTGGGGCTAGTTTAAGTCAAGTGTCACTTTGACTGGGACTACCCAGGAGAGCAGAGAGA	840
Db	781	GTGGGGCTAGTTTAAGTCAAGTGTCACTTTGACTGGGACTACCCAGGAGAGCAGAGAGA	840
OY	841	CGGGGGTAAGTGGGTGCCCGAGCGAGGCTTCCAGCAGACCCAGACAGAACTCTCCAGCAT	900
Db	841	CGGGGGTAAGTGGGTGCCCGAGCGAGGCTTCCAGCAGACCCAGACAGAACTCTCCAGCAT	900
OY	901	CGTGAACCTCCAGCAATGTCCAGCGACAGCAAGCTGGGGCTCTATATGTGTGAAGGCCAACA	960
Db	901	CGTGAACCTCCAGCAATGTCCAGCGACAGCAAGCTGGGGCTCTATATGTGTGAAGGCCAACA	960
OY	961	CGGCAATCCAGCATTTTGGGAGAGACACAGAGGTCAATGTGCATGAAATATCCCTTCATCA	1020
Db	961	CGGCAATCCAGCATTTTGGGAGAGACACAGAGGTCAATGTGCATGAAATATCCCTTCATCA	1020
OY	1021	CGTCAATGGCTCAAAAGACCCATCTGAGGCCACGCGCAGAGACAGAGCTGGTGAACCT	1080
Db	1021	CGTCAATGGCTCAAAAGACCCATCTGAGGCCACGCGCAGAGACAGAGCTGGTGAACCT	1080
OY	1081	GGCGGTAAAGTGGAGAGGTACCGCGGCGGCGAGATTGAGGTACAAAGATGGAAAGG	1140
Db	1081	GGCGGTAAAGTGGAGAGGTACCGCGGCGGCGAGATTGAGGTACAAAGATGGAAAGG	1140
OY	1141	ACTGTCCGGAGCGCACAGTGCACATGCCCTGTGTCTCAAGAGAGGTACACAGAGCGACAC	1200
Db	1141	ACTGTCCGGAGCGCACAGTGCACATGCCCTGTGTCTCAAGAGAGGTACACAGAGCGCGACAC	1200
OY	1201	AGGCAAGCTACAGCCCTGCGGCTGTGGAAATTCGGCTGTGGCTCAGGCGCAATCAAGCTT	1260
Db	1201	AGGCAAGCTACAGCCCTGCGGCTGTGGAAATTCGGCTGTGGCTCAGGCGCAATCAAGCTT	1260
OY	1261	GGAGATCTGGTGTAAATGTCCCGCCCGCAGATATATAGAAAGAGGCTCTCTCCCGACAGAT	1320
Db	1261	GGAGATCTGGTGTAAATGTCCCGCCCGCAGATATATAGAAAGAGGCTCTCTCCCGACAGAT	1320
OY	1321	CTACTCGGTCACAGCGCGGACAGCGCTCAAGCTGCAGAGGCGCTACGAGGGTCCCGCTGCTCT	1380
Db	1321	CTACTCGGTCACAGCGCGGACAGCGCTCAAGCTGCAGAGGCGCTACGAGGGTCCCGCTGCTCT	1380
OY	1381	CAGCATCCAGTGGCACTGGCGGCGCTGTACACACCTGCAGAAATATTGGCCAGCGCTAGTCT	1440
Db	1381	CAGCATCCAGTGGCACTGGCGGCGCTGTACACACCTGCAGAAATATTGGCCAGCGCTAGTCT	1440
OY	1441	CGGGGGGCGGAGACAGTAAAGACTCATATGCATATGATCTGTATCGAGGGGTGTGACAC	1500
Db	1441	CGGGGGGCGGAGACAGTAAAGACTCATATGCATATGATCTGTATCGAGGGGTGTGACAC	1500
OY	1501	GCAGGATCCGCTAAGCCCATATCGAGACCTGTGCACACCTGCAGACGATTTGTGCGAGGAAA	1560
Db	1501	GCAGGATCCGCTAAGCCCATATCGAGACCTGTGCACACCTGTGCAGACGATTTGTGCGAGGAAA	1560
OY	1561	GAAATAGACTGTGAGCAAGCTGTATATCCAGATATCCCAAGCTGTCTGCATATGCAAGTGT	1620
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[illegible]

QY	2701	GTGGAGCTGAAATCTTCATTCATTCAGATGCGCAACCACTTACAGTGTGTCAACTCTCTGGG	2760
DB	2701	GTGGAGGCTAAATCTTCATTCATTCAGATGCGCAACCACTTACAGTGTGTCAACTCTCTGGG	2760
QY	2761	GGCGTGCACAAAGCTCCAGACAGCCCGCTCATATGTATATGTGTGGATGTTCTCAAGTACGGCAA	2820
DB	2761	GGCGTGCACCAAGCTCCAGACAGCCCGCTCATATGTATATGTGTGGATGTTCTCAAGTACGGCAA	2820
QY	2821	CTCTTCACATCTCTCGCGCGCTAAGTGAGAGCACTTCAGCTCTGTGCGCGAAGTCTCC	2880
DB	2821	CTCTTCACATCTCTCGCGCGCTAAGTGAGAGCACTTCAGCTCTGTGCGCGAAGTCTCC	2880
QY	2881	CGACAGCGCGAGACGCTTCGCGTGCATATGTGTAGATGTGGCAGGCTGTGATTCGAGAGCGCGC	2940
DB	2881	CGAGAGGCGCGACGCTTCGCGCTGCATATGTGTAGATGTGGCAGGCTGTGATTCGAGAGCGCGC	2940
QY	2941	GGGAGAGCGACAGAGGCTCTCTTGTGCGCGCTTCGCAACCCGAGAGGCGAGCGCGC	3000
DB	2941	GGGAGAGCGAGACAGAGGCTCTCTTGTGCGCGCTTCGCAACCCGAGAGGCGAGCGCGC	3000
QY	3001	GGGTTCTCGACCAAGAGAGTGTAGAGACTGTGGGTGTGAGCGCGCTGAGCATGTGAAATCT	3060
DB	3001	GGGTTCTCGACCAAGAGAGTGTAGAGACTGTGGGTGTGAGCGCGCTGAGCATGTGAAATCT	3060
QY	3061	TCTCTGTACAGCTTCGACAGTGTGGCGAGAGCGATGGAGTTCTGTGCTTCCGAAAGTGCAT	3120
DB	3061	TCTCTGTACAGCTTCGACAGTGTGGCGAGAGCGATGGAGTTCTGTGCTTCCGAAAGTGCAT	3120
QY	3121	CCACAGACACTGGCTGTCTGGGACATATCTGCTGTGCGAAAGCGAGCTGTGTGAACATCTG	3180
DB	3121	CCACAGAACACTGGCTGTCTGGGAAATATCTGCTGTGCGAAAGCGAGCTGTGTGAACATCTG	3180
QY	3181	TGACTTTGGCTTGGCGCGGACATCTTCAAAACACTGTACTAGTCCGACAGGCGACGTCC	3240
DB	3181	TGACTTTGGCTTGGCGCGGACATCTTCAAAACACTGTACTAGTCCGACAGGCGACGTCC	3240
QY	3241	CTGGCTGCCCCCTGAAGTGGATGGCCCCGTGAAGCATCTTTGACAGAGGTGTACACACGCA	3300
DB	3241	CTGGCTGCCCCCTGAAGTGGATGGCCCCGTGAAGCATCTTTGACAGAGGTGTACACACGCA	3300
QY	3301	GATGACAGATGTGCTTTGGGGTGTCTTCTGGAGATCTTCTCTCTGGGGGCGCTCCCGC	3360
DB	3301	GATGACAGATGTGCTTTGGGGTGTCTTCTGGAGATCTTCTCTCTGGGGGCGCTCCCGC	3360
QY	3361	GTACCCGTGAGTGCAGATCATATGAGAGTGTGTGACAGCGCTGAGAGCGGCAATAGGAT	3420
DB	3361	GTACCCGTGAGTGCAGATCATATGAGAGTGTGTGACAGCGCTGAGAGCGGCAATAGGAT	3420
QY	3421	GAGCGCCCCGAGCTGTGCATCTCCCGCTAATCGCGCATATGTGAATCTGTGTGTGGG	3480
DB	3421	GAGCGCCCCGAGCTGTGCATCTCCCGCTAATCGCGCATATGTGAATCTGTGTGTGGG	3480
QY	3481	AGACCCCAAGGCGCAGACATGCTATCTGTGAGCTGTGTGAGATCTGTGGGCGACTGTCTCA	3540
DB	3481	AGACCCCAAGGCGCAGACATGCTATCTGTGAGCTGTGTGAGATCTGTGGGCGACTGTCTCA	3540
QY	3541	GAGCAGGCGCTCTCAAGAGAGAGAGAGGTCTGTGCATATGGCCCGCGCACTTCTGAGACTC	3600
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QY	3601	AGCAGAGCGCAGCTTCTGTGCAGGTGTGCACATATGGCCCTTACACATATGCCACAGGTACCCG	3660
DB	3601	AGCAGAGCGCAGCTTCTGTGCAGGTGTGCACATATGGCCCTTACACATATGCCACAGGTACCCG	3660
QY	3661	TGAGCAGAGCCCGCAAGCTCTGACAGCGCTACAGCGCTTGGCGATTTACAACTGTGGGT	3720
DB	3661	TGAGCAGAGCCCGCAAGCTCTGACAGCGCTACAGCGCTTGGCGATTTACAACTGTGGGT	3720
QY	3721	GTCTCTTTCGCGAGTGCCTGTGCTACAGAGGACTGTGAGACTGTGTCTCTCGACAGTCAAGAC	3780
DB	3721	GTCTCTTTCGCGAGTGCCTGTGCTACAGAGGACTGTGAGACTGTGTCTCTCGACAGTCAAGAC	3780

Db 721 GTTCCCAAGAGTGGTGGAGTGTGTGTAGAGGAGAGTGGTCTCTGAACTGCACCGT 780
Qy 781 GTGGCGTGAATTTAACTGAGTGTACACTTTGACTGGAGTACCCAGGAGAGGACAGA 840
Db 781 GTGGCGTGAATTTAACTGAGTGTACACTTTGACTGGAGTACCCAGGAGAGGACAGA 840
Qy 841 GAGGCGTGAATGGTGGTGGAGGAGGCGTGGAGAGAGAGAGAGAGAGAGAGAGAGAT 900
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Qy 1081 GCGGATTCAGAGAGTGCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1140
Db 1081 GCGGATTCAGAGAGTGCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1140
Qy 1141 ACTGTCGCGGAT 1200
Db 1141 ACTGTCGCGGAT 1200
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Qy 1801 GGTGAGTGGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1860
Db 1801 GGTGAGTGGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1860

Qy 1861 TGTGTTGGCAGCCCTCTGGCCGAGAGAGAGAGAGAGAGAGAGAGAGAT 1920
Db 1861 TGTGTTGGCAGCCCTCTGGCCGAGAGAGAGAGAGAGAGAGAGAGAGAT 1920
Qy 1921 CAGCTGAGCTGAGTATCCCGCGGTGGCGGAGAGAGAGAGAGAGAGAT 1980
Db 1921 CAGCTGAGCTGAGTATCCCGCGGTGGCGGAGAGAGAGAGAGAGAT 1980
Qy 1981 AGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 2040
Db 1981 AGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 2040
Qy 2041 CTTGAT 2100
Db 2041 CTTGAT 2100
Qy 2101 GCTGAGTGGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAT 2160
Db 2101 GCTGAGTGGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAT 2160
Qy 2161 GGAAGTGGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 2220
Db 2161 GGAAGTGGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 2220
Qy 2221 CATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 2280
Db 2221 CATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 2280
Qy 2281 GGTGAGTGGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAT 2340
Db 2281 GGTGAGTGGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAT 2340
Qy 2341 GGAAGTGGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 2400
Db 2341 GGAAGTGGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 2400
Qy 2401 CTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 2460
Db 2401 CTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 2460
Qy 2461 CATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 2520
Db 2461 CATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 2520
Qy 2521 TGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 2580
Db 2521 TGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 2580
Qy 2581 GGTGAGTGGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAT 2640
Db 2581 GGTGAGTGGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAT 2640
Qy 2641 CAGTGAATTCAGAGAGTGCAGGAGAGAGAGAGAGAGAGAT 2700
Db 2641 CAGTGAATTCAGAGAGTGCAGGAGAGAGAGAGAGAGAGAT 2700
Qy 2701 GTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 2760
Db 2701 GTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 2760
Qy 2761 GGTGAGTGGCTTGAAGAGAGAGAGAGAGAGAGAGAGAT 2820
Db 2761 GGTGAGTGGCTTGAAGAGAGAGAGAGAGAGAGAGAGAT 2820
Qy 2821 CTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 2880
Db 2821 CTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 2880
Qy 2881 GGAAGTGGTGGAGAGAGAGAGAGAGAGAGAGAGAGAT 2940
Db 2881 GGAAGTGGTGGAGAGAGAGAGAGAGAGAGAGAGAGAT 2940

QY 2161 GAAAGAGCTGAGAGAAAGTCTGAGTGGAGTGGAGTGCAGACAGAGCTAG 2220
 DB 2161 GAAAGAGCTGAGAGAAAGTCTGAGTGGAGTGGAGTGCAGACAGAGCTAG 2220
 QY 2221 GATTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGAG 2280
 DB 2221 GATTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGAG 2280
 QY 2281 GAGTTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 2340
 DB 2281 GAGTTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 2340
 QY 2341 GAGTTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 2400
 DB 2341 GAGTTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 2400
 QY 2401 GATTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 2460
 DB 2401 GATTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 2460
 QY 2461 GATTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 2520
 DB 2461 GATTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 2520
 QY 2521 GATTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 2580
 DB 2521 GATTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 2580
 QY 2581 GATTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 2640
 DB 2581 GATTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 2640
 QY 2641 GATTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 2700
 DB 2641 GATTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 2700
 QY 2701 GATTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 2760
 DB 2701 GATTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 2760
 QY 2761 GATTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 2820
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 QY 2821 GATTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 2880
 DB 2821 GATTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 2880
 QY 2881 GATTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 2940
 DB 2881 GATTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 2940
 QY 2941 GATTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 3000
 DB 2941 GATTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 3000
 QY 3001 GATTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 3060
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 QY 3061 GATTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 3120
 DB 3061 GATTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 3120
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 DB 3121 GATTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 3180
 QY 3181 GATTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 3240
 DB 3181 GATTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 3240
 QY 3241 GATTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 3300
 DB 3241 GATTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 3300

DB 3241 CGGCTGCTCTGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 3300
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 DB 3301 GATTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 3360
 QY 3361 GATTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 3420
 DB 3361 GATTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 3420
 QY 3421 GATTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 3480
 DB 3421 GATTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 3480
 QY 3481 GATTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 3540
 DB 3481 GATTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 3540
 QY 3541 GATTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 3600
 DB 3541 GATTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 3600
 QY 3601 GATTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 3660
 DB 3601 GATTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 3660
 QY 3661 GATTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 3720
 DB 3661 GATTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 3720
 QY 3721 GATTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 3780
 DB 3721 GATTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 3780
 QY 3781 GATTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 3840
 DB 3781 GATTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 3840
 QY 3841 GATTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 3900
 DB 3841 GATTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 3900
 QY 3901 GATTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 3960
 DB 3901 GATTCAGAGCTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 3960

RESULT 7
 AAT03090
 ID AAT03090 standard: DNM: 4425 BP.
 XX
 AC AAT03090:
 XX
 DT 14-FEB-1996 (first entry)
 XX
 DE Protein tyrosine-kinase SAL-SI gene.
 KW Protein tyrosine-kinase; PTK; SAL-SI; agonist; cell growth;
 XX differential; ss.
 OS Homo sapiens.
 XX
 FH Key
 FT CDS location/qualifiers
 FT 30..3927
 FT /*tag= a
 FT sig_peptide 30..102
 FT /*tag= b
 FT mat_peptide 103..3924
 FT /*tag= c
 XX
 PN W09527061-A1.

RESULT 9
AAT12068
ID AAT12068 standard; DNA; 4195 BP

[illegible]

Query Match	95.18;	Score 3910.8;	DB 17;	Length 4195;
Best local Similarity	99.98;	Pred. No. 0;		
Matches 3912; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

OY	1	CCGCGGAGAGGGGCGGAGATCGACAGCGGGGGCGCGCGCTGTCCTGGAGACTGGGCTGTG	60
Db	1	CCACGGCGAGGGCGGGAGATCGACAGCGGGGGCGCGCGCTGTGGCTGTGCAATGGGCTGTG	60
OY	61	CGTGGAGACTCTGGAGCGGCGCTGGTGTAGTGGCTACTTCATCAACCCCCCGGACCTTAAACAT	120
Db	61	CGTGGAGACTCTGGAGCGGCGCTGTGTAGTGGCTACTTCATCAACCCCCCGGACCTTAAACAT	120
OY	121	CACGAGGAGTCAACAGCTATCGACACCGGTGACAGAGCTGTGCATCTCTCTGAGGGGACA	180
Db	121	CACGAGGAGTCAACAGCTATCGACACCGGTGACAGAGCTGTGCATCTCTCTGAGGGGACA	180
OY	181	GCACCCCTCGAGTGGGGCTTGGCCGAGAGCTCGAGAGGGGCCAGCCACCGGAGACAAAGA	240
Db	181	GCACCCCTCGAGTGGGGCTTGGCCGAGAGCTCGAGAGGGGCCAGCCACCGGAGACAAAGA	240
OY	241	CACCGAGACACGGGGGTGGTCCGAGATCGAGGGGACAGACCGCCAGCGCCCTACTGGCA	300
Db	241	CACCGAGACACGGGGGTGGTCCGAGATCGAGGGGACAGACCGCCAGCGCCCTACTGGCA	300
OY	301	GGTGTGTCTGTGACGAGGCTACATGCCAAGCAGCACAGGAGCTATCTCTCTACTACAA	360
Db	301	GGTGTGTCTGTGACGAGGCTACATGCCAAGCAGCACAGGAGCTATCTCTCTACTACAA	360
OY	361	GTCATCAACAGGACGCTGAGAGGACACCGCGCGCGCACTCTACTGTTCGTAGAGA	420
Db	361	GTCATCAACAGGACGCTGAGAGGACACCGCGCGCGCACTCTACTGTTCGTAGAGA	420
OY	421	CTTTAGAGACATCATCAAAAGGCTTACAGCGCTTGGTCAGACAGAGAGAGCGCAT	480
Db	421	CTTTAGAGACATCATCAAAAGGCTTACAGCGCTTGGTCAGACAGAGAGAGCGCAT	480
OY	481	GTCGGTGCCTGTCTGTATTCATCCCGCGCTCAATGTCAACGGTGGCGTGCAGAAAGTC	540
Db	481	GTCGGTGCCTGTCTGTATTCATCCCGCGCTCAATGTCAACGGTGGCGTGCAGAAAGTC	540
OY	541	GGTGTGTGACAGAGGCGCAGAGGTTGGTGGCATGACCGCGCGGGCATGCTGTGTC	600
Db	541	GGTGTGTGACAGAGGCGCAGAGGTTGGTGGCATGACCGCGCGGGCATGCTGTGTC	600
OY	601	CAGCGCATGTGTGACGATGCCCTGTATCTGTGAGTGGAGGACACACACTGGGAGACACAGA	660
Db	601	CAGCGCATGTGTGACGATGCCCTGTATCTGTGAGTGGAGGACACACACTGGGAGACACAGA	660
OY	661	CTTCTCTTCCCAACCCCTCTCTGTGTGACATCAACGCAACAGGCTATATATATCCACT	720
Db	661	CTTCTCTTCCCAACCCCTCTCTGTGTGACATCAACGCAACAGGCTATATATATCCACT	720
OY	721	GTTGCCACGAGAGTGGCTGGAGCTGTCTGTAGGGGAGAAAGTGTCTCTTAATGCAACGT	780
Db	721	GTTGCCACGAGAGTGGCTGGAGCTGTCTGTAGGGGAGAAAGTGTCTCTTAATGCAACGT	780
OY	781	GTCGGCTGAGTTAACTCAGGTGTCACTTTCATGGGACTTACCTACGAGAGATGAGCAGA	840
Db	781	GTCGGCTGAGTTAACTCAGGTGTCACTTTCATGGGACTTACCTACGAGAGATGAGCAGA	840

Dk 781 GTGGGCTAG:1TTAACTCAGGTGTCACCTTTGACTTGGACTACCCAGGGAAGGAGGAGCA 840
Qy 841 GCGGGGTAGTGGGGTGGCGAGAGCGCTTGGCAGACAGCACACAACTCTCCAGCAT 900
Db 841 GCGGGGTAGTGGGGTGGCGAGAGCGCTTGGCAGACAGCACACAACTCTCCAGCAT 900
Qy 901 GCTGACATTCACAAAGCTCAGCCAGCAGCACTGGGATGTGATGTGGAGGCGCAAA 960
Db 901 GCTGACATTCACAAAGCTCAGCCAGCAGCACTGGGATGTGATGTGGAGGCGCAAA 960
Qy 961 GCGCATCCAGCGCATTTGGGAGAGAGCAGCGAGGTGATT:1TGCATGAATTCCTTCATCG 1020
Db 961 GCGCATCCAGCGCATTTGGGAGAGAGCAGCGAGGTGATT:1TGCATGAATTCCTTCATCG 1020
Qy 1021 GCTCGAGTGTCTCAAAAGAGCCCATCTGAGAGCCAGCGCAGAGAGAGAGTGTGTAGCT 1080
Db 1021 GCTCGAGTGTCTCAAAAGAGCCCATCTGAGAGCCAGCGCAGAGAGAGTGTGTAGCT 1080
Qy 1081 GCGCGGTGAAGCTGCGAGCGTACCCCGCGCGAGTTGCAGTGTGACAGCATGGAAAGCC 1140
Db 1081 GCGCGGTGAAGCTGCGAGCGTACCCCGCGCGAGTTGCAGTGTGACAGCATGGAAAGCC 1140
Qy 1141 ACTGTCCGAGGAGAGAGTCCACATGCGCTGATGCTCAAGAGGTGACAGAGCCAGCAG 1200
Db 1141 ACTGTCCGAGGAGAGAGTCCACATGCGCTGATGCTCAAGAGGTGACAGAGCCAGCAG 1200
Qy 1201 AAGGATCTTAAAGCTGCGCTGTGAGAGTCCGCTGCTGGCTGAGAGGCGCACTAGCT 1260
Db 1201 AAGGATCTTAAAGCTGCGCTGTGAGAGTCCGCTGCTGGCTGAGAGGCGCACTAGCT 1260
Qy 1261 GAGAGTGTGAGATGTGCCCGCCAGATACATGAGAGAGAGAGAGAGAGAGAGAGAG 1320
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Db 1321 CTACTGCGCTACAGAGCCGCGCCTCAGCTGACAGAGAGAGAGAGAGAGAGAGAGAG 1380
Qy 1381 CAGCATCCAGTGGAGTGGGCGCTGGAGAGCCCTGGAGAGAGAGAGAGAGAGAGAGAG 1440
Db 1381 CAGCATCCAGTGGAGTGGGCGCTGGAGAGCCCTGGAGAGAGAGAGAGAGAGAGAGAG 1440
Qy 1441 CCGGCGCGCGCGAG 1500
Db 1441 CCGGCGCGCGCGAG 1500
Qy 1501 GATAGATGCGGTGAG 1560
Db 1501 GATAGATGCGGTGAG 1560
Qy 1561 GATAGATGCGGTGAG 1620
Db 1561 GATAGATGCGGTGAG 1620
Qy 1621 TGTGTCTCCAAAGAGTGGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
Db 1621 TGTGTCTCCAAAGAGTGGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
Qy 1681 GCGCGAGGAG 1740
Db 1681 GCGCGAGGAG 1740
Qy 1741 GCTCTGAGTGTGAG 1800
Db 1741 GCTCTGAGTGTGAG 1800
Qy 1801 GCTCTGAGTGTGAG 1860
Db 1801 GCTCTGAGTGTGAG 1860
Qy 1861 TGTGTCTCCAAAGAGTGGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
Db 1861 TGTGTCTCCAAAGAGTGGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920

Qy 1921 CAGGCTCAGCTGAGTATCCCCCGGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
Db 1921 CAGGCTCAGCTGAGTATCCCCCGGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
Qy 1981 AGTGAAG 2040
Db 1981 AGTGAAG 2040
Qy 2041 CTTGAG 2100
Db 2041 CTTGAG 2100
Qy 2101 GCTGAG 2160
Db 2101 GCTGAG 2160
Qy 2161 GAG 2220
Db 2161 GAG 2220
Qy 2221 CATCAG 2280
Db 2221 CATCAG 2280
Qy 2281 GCGCTGCTCACTGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2340
Db 2281 GCGCTGCTCACTGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2340
Qy 2341 GAG 2400
Db 2341 GAG 2400
Qy 2401 CTTGATCTTCTTAAAG 2460
Db 2401 CTTGATCTTCTTAAAG 2460
Qy 2461 CATCATCATGAG 2520
Db 2461 CATCATCATGAG 2520
Qy 2521 TGGCAGCAG 2580
Db 2521 TGGCAGCAG 2580
Qy 2581 GCGCTTGGAG 2640
Db 2581 GCGCTTGGAG 2640
Qy 2641 CAGCGTGGAG 2700
Db 2641 CAGCGTGGAG 2700
Qy 2701 GTCGAG 2760
Db 2701 GTCGAG 2760
Qy 2761 GCGGTGAG 2820
Db 2761 GCGGTGAG 2820
Qy 2821 CCGTCTCACTTCTGCGAG 2880
Db 2821 CCGTCTCACTTCTGCGAG 2880
Qy 2881 GAG 2940
Db 2881 GAG 2940
Qy 2941 GGGGAG 3000
Db 2941 GGGGAG 3000

AC AAC49753;
 XX
 D: 10-MAR-1994 (first entry)
 XX
 DE PTK gene SAL-S1.
 XX
 KW PTK; protein tyrosine kinase; catalytic domain; c-kit; FLT/FLK;
 KW fetal liver kinase; megakaryocyte; amplification; primer;
 KW polymerase chain reaction; PCR; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key location/qualifiers
 FH CDS complement (1877..2923)
 FT /*tag- a
 FT misc_difference 3026
 FT /*tag- b
 FT /*note- "base labelled as X in the specification"
 FT /*tag- c
 FT /*note- "base illegible in the specification"
 FT misc_difference 5693..5700
 FT /*tag- d
 FT /*note- "bases illegible in the specification"
 FN W0315201-A.
 ED 05-AUG-1993.
 XX
 PE 22-JAN-1993; 93WD-0500586.
 XX
 PR 22-JAN-1992; 92US-0826935.
 XX
 EA (NEML-) NEW ENGLAND DEACOMFESS HOSPITAL.
 XX
 PI Avraham H, Cowley S, Groopman J, Scadden D;
 DR WPI: 1993-120336/40.
 DR P-FSDB; AAK41542.
 XX
 PI New protein tyrosine kinase genes and proteins encoded by genes -
 PT are of human mega-karyocytic origin
 XX
 PS Claim 2: Fig 4; 60pp; English.
 XX
 CC PTK genes were identified using two sets of degenerative
 CC oligonucleotide primers: a first set which amplifies all PTK DNA
 CC segments (AA049743-44), and a second set which amplifies highly
 CC conserved sequences present in the catalytic domain of the c-kit
 CC subgroup of PTKs (AA049745-46). The PTK genes identified are described
 CC in AA049747-57 and AAK41542-52.
 CC SAL-S1 is expressed in several megakaryocytic cell lines, but not
 CC in erythroid cell lines. The SAL-S1 expression prod. exhibited
 CC significant sequence homology with known protein tyrosine kinases
 CC of the FLT/FLK family. The partial and full-length SAL-S1 gene
 CC sequences are given in AA049747 and AA049753 respectively.
 XX
 SO Sequence 6827 BP; 1555 A; 1868 C; 1740 G; 1660 T; 4 other;
 Query Match 25.3%; Score 1040.2; DB 14; Length 6827;
 Best local Similarity 38.3%; Prod. No. 2.1e-199;
 Matches 1051; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

DB 2827 GCGGGCTTCGAGAGACCGAGGCGGAGCGGCGGGCTTCTCCAGACCAAGAGCTGAG 2768
 QY 3026 GACCTGGCTAGACGCCCGCTGACCATGAGATCTGTGCTNAGCTTCCAGCTGGCC 3085
 DB 2767 GACCTGGCTAGACGCCCGCTGACCATGAGATCTGTGCTNAGCTTCCAGCTGGCC 2708
 QY 3086 AGAGGATGACATCTTCCGTTCCGAAAGTGCATGCACAGAGACCTGGCTGCGGAGC 3145
 DB 2707 AGAGGATGACATCTTCCGTTCCGAAAGTGCATGCACAGAGACCTGGCTGCGGAGC 2648
 QY 3146 ATTCTGCTCGAAAGCGACGTGGTGAAGATCTGTGACTTTGGCTTCCCGGAGATC 3205
 DB 2647 ATTCTGCTCGAAAGCGACGTGGTGAAGATCTGTGACTTTGGCTTCCCGGAGATC 2588
 QY 3206 TACAAAGACCTGACTAGTCTCCGCAAGGCGATGCCCCGCTCCCTTAAATGATGCGC 3265
 DB 2587 TACAAAGACCTGACTAGTCTCCGCAAGGCGATGCCCCGCTCCCTTAAATGATGCGC 2528
 QY 3266 CCTGAAAGCATCTCGACAGAGGTGTACACACGACAGTGAAGTGTGCTTGGGGTG 3325
 DB 2527 CCTGAAAGCATCTCGACAGAGGTGTACACACGACAGTGAAGTGTGCTTGGGGTG 2468
 QY 3326 CTCTCTGGAGATCTCTCTCTGGGGGCTTCCCGTTACCTGCGGCTGCAGATCAATGAG 3385
 DB 2467 CTCTCTGGAGATCTCTCTCTGGGGGCTTCCCGTTACCTGCGGCTGCAGATCAATGAG 2408
 QY 3386 GAGTCTCCGAGCGCTGAGAGACGCGACAAAGATGAGGGCCCGGAGCTGTGCACTCC 3445
 DB 2407 GAGTCTCCGAGCGCTGAGAGACGCGACAAAGATGAGGGCCCGGAGCTGTGCACTCC 2348
 QY 3446 GCCATAGCCCGCATATGCTGACCTGTGCTCCGAGACCCCAAGCGAGCTGCATTC 3505
 DB 2347 GCCATAGCTGCTATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 2288
 QY 3506 TCGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3565
 DB 2287 TCGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2228
 QY 3566 GAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3625
 DB 2227 GAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2168
 QY 3626 TCGACCATGCGCCCTACATGATGCGCCAGGCTGACGAGAGAGCGCCGCAAGCTGACAG 3685
 DB 2167 TCGACCATGCGCCCTACATGATGCGCCAGGCTGACGAGAGAGCGCCGCAAGCTGACAG 2108
 QY 3686 CGCCAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3745
 DB 2107 CGCCAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2048
 QY 3746 GGGGCTGAGACCGCGTGTCTCTCCAGATTAACATTTTGAAGAAATTCCTATGACCCCA 3805
 DB 2047 GGGGCTGAGACCGCGTGTCTCTCCAGATTAACATTTTGAAGAAATTCCTATGACCCCA 1988
 QY 3806 ACGACCTAAGAGCTCTGTGAGACACAGACAGAGAGTGGATGCTGCTGCTGCGAG 3865
 DB 1987 ACGACCTAAGAGCTCTGTGAGACACAGACAGAGAGTGGATGCTGCTGCTGCGAG 1928
 QY 3866 GAGTTGAGCAATAGAGAGCGCATATGCAAGAAAGCGGCTTACGCT 3914
 DB 1927 GAGTTGAGCAATAGAGAGCGCATATGCAAGAAAGCGGCTTACGCT 1879
 RESULT 13
 AAT03101/c
 ID AAT03101 standard; DNA; 6827 BP.
 XX
 AC AAT03101;
 XX
 DT 14-FEB-1996 (first entry)
 XX
 DE Protein tyrosine kinase SAL-S1 gene.
 XX

[illegible]

PR 31-021-1994: 54US-0252498.
 PR 15-FEB-1996: 54US-0601891.
 XX (CYPR) UNL FRINCEYON.
 RA
 XX
 PT Lemischka CK;
 XX
 DR WPI: 1999 35/194/30.
 XX P-PSDB: MAY08618.
 XX
 PT Isolating hematopoietic cells expressing fetal liver kinase 1
 PT receptors
 XX
 PS Disclosure: Fig 2; 59pp; English.
 XX
 CC This invention describes a novel method of isolating cells expressing
 CC fetal liver kinase 1 (Flk-1) receptors on their surface and comprises
 CC binding the cells to a polyclonal or monoclonal antibody specific to
 CC the Flk-1 receptor and isolating the cells that have bound to the
 CC antibody. The method can be used to isolate hematopoietic stem cells in
 CC any mammal but preferably a rat, mouse, rabbit or human. The proteins of
 CC the invention belong to the receptor protein family. This sequence
 CC encodes the murine Flk-1 protein which is used in the method of the
 CC invention.
 CC
 XX
 SO Sequence 5404 BP: 1411 A: 1297 C: 1423 G: 1273 T: 9 other:
 Query Match: 27.38; Score 713; EB 20; Length 5404;
 Best Local Similarity 54.58; Pred. No. 1,13-133;
 Matches 1711; Conservative 0; Mismatches 1345; Indels 81; Gaps 11;

DB 1234 GAAACCA---CACTGGGCACTCAAGTCCGAATCCCTGTAAGTATCTGATGCCAGCT 1290
 QY 1109 CCCGAGTCCAGTGTAGCAAGATGAAAGGCACCTGCCGGCGCACA-----GT 1159
 DB 1291 CCTGATATCAAAATGGTACAGAAATGGAAGGCCCATTTAGTCTCACTACACATGATTGTT 1350
 QY 1160 CCACATGCCCTGTGTCTCAAGAGAGTACAGAGAGGCCACAGGACCTCAACCTCGCC 1219
 DB 1351 GGGCATGAATCAACCATATGAGTGAAGTGAAGATGAGAGGAACTACACCTGATC 1410
 QY 1220 CTGTGAACCTCCGCTGTGGCTGAGGCGCAACATAGCTGAGCTGTGGTGAATGTT 1279
 DB 1411 CTCACCAACCCCATTTCAATGAGAGAAACAGCCACATATGTTCTCTGTGTAATGTC 1470
 QY 1280 CCCCCCAGATACATGAGAGAGGAGGCTCCTCCCA---GCATCTACTCGCTGCACAG 1336
 DB 1471 CCACGCCAGATGAGTGAAGAAAGCCCTGATCTGCCCTATGATCTTCTACAGTATGGAGC 1530
 QY 1337 CGCCAGGCCCTCACTGACAGGCGCTACGGGGTCCCTCTCTTACATCTCAGTGGAC 1396
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 REFERENCE 1 (bases 1 to 4416)
 AUTHORS Aprelikova, O.
 JOURNAL Direct Submission
 Submitted (07-SEP-1992) U. Aprelikova, University of Helsinki, Cancer Biology Laboratory, Dept. of Pathology, Haartmaninkatu 3, 00290 Helsinki, FINLAND
 REFERENCE 2 (bases 1 to 4416)
 AUTHORS Aprelikova, O., Pajusola, K., Parlane, J., Armstrong, E., Allalio, R., Bailey, S. K., McMahon, J., Masumoto, J., Huebner, K. and Allalio, K.
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661 CTTCTTTCACACCCCTTCTGTGTGACATGACAGGACAGCTGTATGATCAGCT 720
DB 663 CTTCTTTCACACCCCTTCTGTGTGACATGACAGGACAGCTGTATGATCAGCT 722
721 GTTGCCGAGGAAGTGTGAGAGCTGTGTGAGGGAGAAAGTGTGCTGATGACAGCT 780
DB 723 GTTGCCGAGGAAGTGTGAGAGCTGTGTGAGGGAGAAAGTGTGCTGATGACAGCT 782
781 GTGGGCTGAGTTTAATCAGGTGTACCTTTGACTGTGAGTACCAAGAGTAGCAGA 840
DB 783 GTGGGCTGAGTTTAATCAGGTGTACCTTTGACTGTGAGTACCAAGAGTAGCAGA 842
841 GGGGGTAACTGGGTGCGGAGGAGAGCTGCCAGAGCCACACAGAGACTCTCCAGCT 900
DB 843 GGGGGTAACTGGGTGCGGAGGAGAGCTGCCAGAGCCACACAGAGACTCTCCAGCT 902
901 CCGTACCATCCACAACTGTGAGGACGAGAGCTGTGATGTGTGCAAGGCCACAGA 960
DB 903 CCGTACCATCCACAACTGTGAGGACGAGAGCTGTGATGTGTGCAAGGCCACAGA 962
961 CCGTACCATCCACAACTGTGAGGACGAGAGCTGTGATGTGTGCAAGGCCACAGA 1020
DB 963 CCGTACCATCCACAACTGTGAGGACGAGAGCTGTGATGTGTGCAAGGCCACAGA 1022
1021 CGTGAGTGTGCTAAAGAGCTTCTGTGAGGCGCACGAGAGAGAGTGTGCAAGCT 1080
DB 1023 CGTGAGTGTGCTAAAGAGCTTCTGTGAGGCGCACGAGAGAGAGTGTGCAAGCT 1082
1081 GCGCGTGAAGCTGTGAGAGCTTCTGTGAGGCGCACGAGAGAGAGTGTGCAAGAGCT 1140
DB 1083 GCGCGTGAAGCTGTGAGAGCTTCTGTGAGGCGCACGAGAGAGAGTGTGCAAGAGCT 1142
1141 ACTGTGCGGGGCGCACAGTCCAGATGCTGTGTGCTCAAGGAGGTGACAGAGGCCAGC 1200
DB 1143 ACTGTGCGGGGCGCACAGTCCAGATGCTGTGTGCTCAAGGAGGTGACAGAGGCCAGC 1202
1201 AGGCACTTACACCTGCTGCTGTGAACTGCTGTGAGGCTGTGAGGCTGTGAGGCT 1260
DB 1203 AGGCACTTACACCTGCTGCTGTGAACTGCTGTGAGGCTGTGAGGCTGTGAGGCT 1262
1261 GAGAGTGTGTGAATGTGCGCCCGAGATACATGAGAGAGGCTGCTGCTGAGAGCT 1320
DB 1263 GAGAGTGTGTGAATGTGCGCCCGAGATACATGAGAGAGGCTGCTGCTGAGAGCT 1322
1321 CTACTGTGCTACAGCGCGGAGGCTTACCTGTACAGGCGCTTACGAGGCTGTGCTGCT 1380
DB 1323 CTACTGTGCTACAGCGCGGAGGCTTACCTGTACAGGCGCTTACGAGGCTGTGCTGCT 1382

QY 1381 CAGCATCCAGTGGGACTGGGCGCCCTGGACACCTCTGCAGATGTTTGCCACGGTAGTCT 1440
 DB 1383 CAGCATCCAGTGGGACTGGGCGCCCTGGACACCTCTGCAGATGTTTGCCACGGTAGTCT 1442
 QY 1441 CCGGCGGGGCGGACGACGACGACCTCATGCGACAGTGGCGTGACTGAGGGCGGGTAGCCAC 1500
 DB 1443 CCGGCGGGGCGGACGACGACGACCTCATGCGACAGTGGCGTGACTGAGGGCGGGTAGCCAC 1502
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 DB 1503 GCGAGATGCGCTTAACCCCATGCGAGAGGCTGGACACCTGGACGACCTTTGGAGGAGAA 1562
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 DB 1623 TGTGTCTCCAAACAGGTGGGCGAGATGAGCGGCTATCTACTTCTATGTAGCCACAT 1682
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 DB 1683 CCGCGAGCGCTTCACCATGGAATCCAGACCATCCGAGAGCTACTAGAGGGCGACCGGT 1742
 QY 1741 GCTGCTGAGCTTCCAAAGCTGACAGCTAGCAAGCAATCTGCGCTGCTACCGCTCAA 1800
 DB 1743 GCTGCTGAGCTTCCAAAGCTGACAGCTAGCAAGCAATCTGCGCTGCTACCGCTCAA 1802
 QY 1801 CCTGCTGAGCTTCCAAAGCTGACAGCTAGCAAGCTAGCAAGCTAGCAAGCTAGCA 1860
 DB 1803 CCTGCTGAGCTTCCAAAGCTGACAGCTAGCAAGCTAGCAAGCTAGCAAGCTAGCA 1862
 QY 1861 TCTGTTGCGCACCCCTCTGGCGCCAGCTGGAGAGGCTGGACACTGGGCGCGCGACGC 1920
 DB 1863 TCTGTTGCGCACCCCTCTGGCGCCAGCTGGAGAGGCTGGACACTGGGCGCGCGACGC 1922
 QY 1921 CAGGCTCAGCTCAGTATCCCGCGCTGCGCTGCGAGACAGAGGGCGACATATGTGCGA 1980
 DB 1923 CAGGCTCAGCTCAGTATCCCGCGCTGCGCTGCGAGACAGAGGGCGACATATGTGCGA 1982
 QY 1981 AGTGCAGAGCGGCGACGCGATGATAGGACCTGGACACATAGCTAGCTGCTGCTAGCG 2040
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 QY 2041 CCGTGCAGAGCGGCGACGCGATGATAGGACCTGGACACATAGCTAGCTGCTGCTAGCG 2100
 DB 2043 CCGTGCAGAGCGGCGACGCGATGATAGGACCTGGACACATAGCTAGCTGCTGCTAGCG 2102
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 DB 2103 GCTGCAGAGCGGCGACGCGATGATAGGACCTGGACACATAGCTAGCTGCTGCTAGCG 2162
 QY 2161 GCGAGAGCGGCGACGCGATGATAGGACCTGGACACATAGCTAGCTGCTGCTAGCG 2220
 DB 2163 GCGAGAGCGGCGACGCGATGATAGGACCTGGACACATAGCTAGCTGCTGCTAGCG 2222
 QY 2221 CAGTGCAGAGCGGCGACGCGATGATAGGACCTGGACACATAGCTAGCTGCTGCTAGCG 2280
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 QY 2281 GCGTGCAGAGCGGCGACGCGATGATAGGACCTGGACACATAGCTAGCTGCTGCTAGCG 2340
 DB 2283 GCGTGCAGAGCGGCGACGCGATGATAGGACCTGGACACATAGCTAGCTGCTGCTAGCG 2342
 QY 2341 GCGAGAGCGGCGACGCGATGATAGGACCTGGACACATAGCTAGCTGCTGCTAGCG 2400
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 QY 2401 CCGTGCAGAGCGGCGACGCGATGATAGGACCTGGACACATAGCTAGCTGCTGCTAGCG 2460
 DB 2403 CCGTGCAGAGCGGCGACGCGATGATAGGACCTGGACACATAGCTAGCTGCTGCTAGCG 2462

QY 2461 CATCATCATGACCCCGGGAGGCTGCTTGGAGGAGCAATGCGAATACCTGCTACGA 2520
 DB 2463 CATCATCATGACCCCGGGAGGCTGCTTGGAGGAGCAATGCGAATACCTGCTACGA 2522
 QY 2521 TGGCAGCAGTGGGAATTTCCCGGAGCGGCTGACCTGGGGAGAGTCTGGAGTACG 2580
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 DB 2643 CACCGTGGCCGTGAAAAATGCTGAAAAAGGGCGCCACGCGCAGCAGCAGCGCCCTGAT 2702
 QY 2701 GTGGAGCTCAAGATCTCTCATTCATTCGGAACCACTCAAGCTGATCAAGCTCTCGG 2760
 DB 2703 GTGGAGCTCAAGATCTCTCATTCATTCGGAACCACTCAAGCTGATCAAGCTCTCGG 2762
 QY 2761 GGGGTGACCAAGGCGGAGGGCGCCCTCATGGTATCTGTGAGTCTGCAAGTACGGCAA 2820
 DB 2763 GGGGTGACCAAGGCGGAGGGCGCCCTCATGGTATCTGTGAGTCTGCAAGTACGGCAA 2822
 QY 2821 CCTCTCAACTTCTGCGCCGCAAGCGGAGCCCTTACGCGCCCTGCGCGAGAGTCTCC 2880
 DB 2823 CCTCTCAACTTCTGCGCGCCCAAGCGGAGCCCTTACGCGCCCTGCGCGAGAGTCTCC 2882
 QY 2881 CAGCAGCGGCGGAGCGCTTCCGCGCCATGTTGAGTGTGCGACAGCTGGATTCGAGCGGCC 2940
 DB 2883 CAGCAGCGGCGGAGCGCTTCCGCGCCATGTTGAGTGTGCGACAGCTGGATTCGAGCGGCC 2942
 QY 2941 GGGGAGCAGGCGAGGCTCTCTTGGCGGCTTCTGCGAAGCAGGAGGGGAGCGAGCGG 3000
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 QY 3001 GGGCTCTCCAGACGACAGAGCTGAGGACCTGTGCGTACGCGCGCTGACCATGGAGATCT 3060
 DB 3003 GGGCTCTCCAGACGACAGAGCTGAGGACCTGTGCGTACGCGCGCTGACCATGGAGATCT 3062
 QY 3061 TGTCTGTACAGCTTCCAGTGGCGCAGAGGATGAGTCTTGTGCTTCCGAAAGTGCAT 3120
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 QY 3121 CCACAGAGAGCTGCTGCTGCGAATCTGTGTGCGAAGCAGGAGTGTGAGATCTG 3180
 DB 3123 CCACAGAGAGCTGCTGCTGCGAATCTGTGTGCGAAGCAGGAGTGTGAGATCTG 3182
 QY 3181 TGACTTTGGCTTGGCGGAGATATCTACAAAGACCTGACTACCTGCGCAAGGGCAGTGC 3240
 DB 3183 TGACTTTGGCTTGGCGGAGATATCTACAAAGACCTGACTACCTGCGCAAGGGCAGTGC 3242
 QY 3241 CCGGCTCCGCTGGAAGTGGATGGCGCTGAAAGCATCTTGACAGAGGTGTACACAGCA 3300
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 QY 3301 GAGTACAGTGTGCTCTTGGGAGTCTCTGCGAGAGTCTCTCTGCGGAGCTTCCG 3360
 DB 3303 GAGTACAGTGTGCTCTTGGGAGTCTCTGCGAGAGTCTCTCTGCGGAGCTTCCG 3362
 QY 3421 GAGGCGCCCGGAGCTGGCCACTCCCGCAATAGCCCGCATATGCTGMACTGCTGCTCGG 3480
 DB 3423 GAGGCGCCCGGAGCTGGCCACTCCCGCAATAGCCCGCATATGCTGMACTGCTGCTCGG 3482
 QY 3481 AGACCCCAAGGCGAGACTGATTCGAGAGCTGGTGGAGATCTGCGGAGCCTGCTCCA 3540
 DB 3483 AGACCCCAAGGCGAGACTGATTCGAGAGCTGGTGGAGATCTGCGGAGCCTGCTCCA 3542
 QY 3541 GCGCAGGGGCTGTCAAGAGAGAGAGGAGCTGTGCAATGCGCCCGCAGCTCTCAAGAGCTC 3600

QY	1400	GGGCGCTGGAGACCCCTGGTAAATGCTTTGGCCAGCGTACGCTCCGCGCGGCGGACAGACAA	1459
Dp	1381	CGGCGCTGGAGACCCCTGGTAAATGCTTTGGCCAGCGTACGCTCCGCGCGGCGGACAGACAA	1440
QY	2446	GAGCTCATGATGCAATGCTCCCGTGGATCGAGCGCGGTATACACCGACATGGCGTGAACCC	1519
Dp	1441	GAGCTCATGATGCAATGCTCCCGTGGATCGAGCGCGGTATACACCGACATGGCGTGAACCC	1500
QY	1520	ATCCAGAGCGCTGGACACCTGGAGCGAGTTTGTGGAGGCGAAGAAATAGACTGTGACAG	1579
Dp	2501	ATCCAGAGCGCTGGACACCTGGAGCGAGTTTGTGGAGGCGAAGAAATAGACTGTGACAG	1560
QY	1580	CTGGTGGATGAGATATCCAAAGCTGTGCTCATATCAAGTGTGTGTCTCCAAACAGGTG	1639
Dp	1561	CTGGTGGATGAGATATCCAAAGCTGTGCTCATATCAAGTGTGTGTCTCCAAACAGGTG	1620
QY	1640	GGCCAGGATATAGCGCTCATCTGACTCATATGAGACCAACCTCCCGAGGCGCTTGACACATC	1699
Dp	1621	GGCCAGGATATAGCGCTCATCTGACTCATATGAGACCAACCTCCCGAGGCGCTTGACACATC	1680
QY	1730	GAATCCAGGCTATCGAGGAGTACTAGAGGCGACAGGCGTACTCTCTGAGCTGTCAAGCC	1759
Dp	1681	GAATCCAGGCTATCGAGGAGTACTAGAGGCGACAGGCGTACTCTCTGAGCTGTCAAGCC	1740
QY	1760	GACAGCTACAAATAGAGACATCTGCGCTGTGATACCGCTCAACCTGTCCACGCTGCACAT	1819
Dp	1741	GACAGCTACAAATAGAGACATCTGCGCTGTGATACCGCTCAACCTGTCCACGCTGCACAT	1800
QY	1820	GGGACAGGAGACCGCTGTCTGCTGACCTCCAAAGCTGTATCTTTGGCACCCCTGTG	1879
Dp	1801	GGGACAGGAGACCGCTGTCTGCTGACCTCCAAAGCTGTATCTTTGGCACCCCTGTG	1860
QY	1880	GGGCGCAGCTGTGAGAGGTTGGCACTTGGAGGAGCGGCGACGCGCAAGCTGAGTATC	1939
Dp	1861	GGGCGCAGCTGTGAGAGGTTGGCACTTGGAGGAGCGGCGACGCGCAAGCTGAGTATC	1920
QY	1940	GGGCGCGCTGGCGCCCGAGACATGAGAGCGCCCATGTGTGTATGATCCAAAGCGCGGCGAC	1999
Dp	1921	GGGCGCGCTGGCGCCCGAGACATGAGAGCGCCCATGTGTGTATGATCCAAAGCGCGGCGAC	1980
QY	2000	CATGCAAGACATCCGACAGAAAGTATCTTGGCGAGCGCTGGAAACCCCTCGCGTC	2059
Dp	1981	CATGCAAGACATCCGACAGAAAGTATCTTGGCGAGCGCTGGAAACCCCTCGCGTC	2040
QY	2060	AAGCGAAGATATACCAATCTCCCTGGTGAACGTGAAGCATATCTGGACATGCACTGCTG	2119
Dp	2041	AAGCGAAGATATACCAATCTCCCTGGTGAACGTGAAGCATATCTGGACATGCACTGCTG	2100
QY	2120	GTGGTGGGAGTATAGCGCCCGACATCTGTGTGTATCAAGAGCAAGAGCTGTGTGGAGAA	2179
Dp	2101	GTGGTGGGAGTATAGCGCCCGACATCTGTGTGTATCAAGAGCAAGAGCTGTGTGGAGAA	2160
QY	2180	AAGCTTGGACTGACTTGGCGGACTCAATCCGAAGCTGAGCATCCACCGGCTGGCGAG	2239
Dp	2161	AAGCTTGGACTGACTTGGCGGACTCAATCCGAAGCTGAGCATCCACCGGCTGGCGAG	2220
QY	2240	GAGCATGGGAGAGCTATCTGTGCAGCTGTGCANAGCTCAAGGCGCTGCTCAACTCTTC	2299
Dp	2221	GAGCATGGGAGAGCTATCTGTGCAGCTGTGTGCANAGCTCAAGGCGCTGCTCAACTCTTC	2280
QY	2300	GGGACCGTGGATGGAGAGCTCGCAGAGATTAAGGGCGAGCTGGAGATGTGTATCTTTGTC	2359
Dp	2281	GGGACCGTGGATGGAGAGCTCGCAGAGATTAAGGGCGAGCTGGAGATGTGTATCTTTGTC	2340
QY	2360	GGTACCGGCTCATATGCTGTCTTCTTGTGGTCTCTCTCTCTCATCTTCTGTAAATG	2419
Dp	2341	GGTACCGGCTCATATGCTGTCTTCTTGTGGTCTCTCTCTCTCATCTTCTGTAAATG	2400
QY	2420	AGGAGCGCGCGCCAGGACAGATCAAGACGGGCTACCTGTCCATCATATCATGAGACCCGGG	2479
Dp	2401	AGGAGCGCGCGCCAGGACAGATCAAGACGGGCTACCTGTCCATCATATCATGAGACCCGGG	2460

QY	2480	GAGGTGCTCTGGAGAGGACAAATCCGAATACCTGCTACGATCTCCAGCCAGCGGAATTC	2539
Db	2461	GAGGTGCTCTGGAGAGGACAAATCCGAATACCTGCTACGATCTCCAGCCAGCGGAATTC	2520
QY	2540	CCCCGAGAGCGGCTGACACCTGGGGAGAGTGTCTGGCTACGGTGCCCTTGGGAAGTGGTG	2599
Db	2521	CCCCGAGAGCGGCTGACACCTGGGGAGAGTGTCTGGCTACGGTGCCCTTGGGAAGTGGTG	2580
QY	2600	GAAAGCTCGCTTTGCGGATCTCCACAAAGGGACAGACTGTACACCCCTGGCCGTGAAAATG	2659
Db	2581	GAAAGCTCGCTTTGCGGATCTCCACAAAGGGACAGACTGTACACCCCTGGCCGTGAAAATG	2640
QY	2660	CTAAAGAGAGGCGCACGGGCGACCGAGACACGGCGGCTGATGTGCGAGGTCAAGATCTTC	2719
Db	2641	CTAAAGAGAGGCGCACGGGCGACCGAGAGCGCGGCTGATGTGCGAGGTCAAGATCTTC	2700
QY	2720	ATTACATCGGCACACCACTCAACGTGTCTCAACCTCTCTGGGGCTGTACCAAGCCGCTAG	2779
Db	2701	ATTACATCGGCACACCACTCAACGTGTCTCAACCTCTCTGGGGCTGTACCAAGCCGCTAG	2760
QY	2780	GCGCCCTCATATGATGATCGGGAGTGTCTGCAAGTACGGCAACCTCTCCAACTTCTGTGGC	2839
Db	2761	GCGCCCTCATATGATGATGATGAGGTGTCTGCAAGTACGGCAACCTCTCCAACTTCTGTGGC	2820
QY	2840	GCCCAAGCGGAGCGCCTTACAGCCCTGCGGGAGAAAGTGTCCCGAGACGCGGAGCTTC	2899
Db	2821	GCCCAAGCGGAGCGCCTTACAGCCCTGCGGGAGAAAGTGTCCCGAGACGCGGAGCTTC	2880
QY	2900	CGGCGCATGTGTGAGACTGCGCAGGCTGTGATCTGGAGAGCGGCTGGGAGACAGCCACAGGTC	2959
Db	2881	CGGCGCATGTGTGAGACTGCGCAGGCTGTGATCTGGAGAGCGGCTGGGAGACAGCCACAGGTC	2940
QY	2960	CTCTTGCGCGGTTCTGCAAGACCGAGGCGGAGACGAGGCGGGCTTCTCCAAACCAACAA	3019
Db	2941	CTCTTGCGCGGTTCTGCAAGACCGAGGCGGAGACGAGGCGGGCTTCTCCAAACCAACAA	3000
QY	3020	CGTGAGAGACTGTGCTGCTGAGCGCCCTGACCATGGAAGATCTTGTCTCTACAGCTTCCAG	3079
Db	3001	GCTGAGAGACTGTGCTGCTGAGCGCGCTACCATGGAAGATCTTGTCTCTACAGCTTCCAG	3060
QY	3080	GTTGGCCAGAGGATGGAATTTCTCTGSGCTTCCCAAGTGCATCCACAGACCTGATCTCT	3139
Db	3061	GTTGGCCAGAGGATGGAATTTCTCTGSGCTTCCCAAGTGCATCCACAGACCTGATCTCT	3120
QY	3140	CGGACATCTCTCTGCTGGAAGAGCGAGCTGATGGAAGATCTGTGACTTGTGGCTTGCCCGG	3199
Db	3121	CGGACATCTCTCTGCTGGAAGAGCGAGCTGATGGAAGATCTGTGACTTGTGGCTTGCCCGG	3180
QY	3200	GACATCTACAAAGACCCCTGACTAATGTCCGCAAGGCGATGCGCCGGCTGCCCTCGAAAGTG	3259
Db	3181	GACATCTACAAAGACCCCGACTAGCTCCGAGGGCGCATGCGCGGCTGCCCTCGAAAGTG	3240
QY	3260	ATGAGCCCTGAAAGCATTTTGACAGAGGTGTACACACGCGAGATGACGTGTGATCTTT	3319
Db	3241	ATGAGCCCTGAAAGCATTTTGACAAAGGTGTACACACGCGAGATGACGTGTGATCTTT	3300
QY	3320	GGGGTGCTTCTGTGGAGATCTTCTCTCTGAGGGCGCTCCCGTACCTGTGGGTGACATG	3379
Db	3301	GGGGTGCTTCTGTGGAGATCTTCTCTCTGAGGGCGCTCCCGTACCTGTGGGTGACATG	3360
QY	3380	AATAGAGACTGTGCGACCGGCTGAGAGAGGACAAAGATGAGAGGCGCCCGACGCTGCGC	3439
Db	3361	AATAGAGACTGTGCGACCGGCTGAGAGAGGACAAAGATGAGAGGCGCCCGAGGCTGCGC	3420
QY	3440	ACTCGCGCATACGCCCGCATATGCTGAACTGTGTGCGGAGACCCCAAGGCGAGACT	3499
Db	3421	ACTCGCGCATACGCCCGCATATCTGAACTGTGTGCGGAGACCCCAAGGCGAGACT	3480
QY	3500	GCAATCTCGGAGCTGTGTGAGATCTCTGAGGAGACCTGTCTCAGAGGCGAGGGCGCTGCAGAG	3559
Db	3481	GCAATCTCGGAGCTGTGTGAGATCTCTGAGGAGACCTGTCTCAGAGGCGAGGGCGCTGCAGAG	3540
QY	3560	CAAGAGAGTGTGATGAGCCCCCGCAGCTCTCAGAGCTCAGAAAGGGCGACCTTCTCG	3619

Db 866 GCGGAGCTAGGTTAGTACCTGAGGCGGCTTCCAGAGACCCGACAGAACTCTCCAGCAT 925
Qy 901 CCGTACATCCACAACTGAGGCGAGACAGACCTGGAGTGTATGTGGACAGGCGCAACA 960
Db 926 CCGTACATCCACAACTGAGGCGAGAACTGAGGCGGCTATGTGTGAGGCGCAACA 985
Qy 961 CCGTACATCCACAACTGAGGCGAGACAGACCTGGAGTGTATGTGGACAGGCGCAACA 1020
Db 986 TGGATTCAGAGGCTTCCGAGAAACAGACAGGTCATTTGACCAAAAAGCCCTTATCAG 1045
Qy 1021 CCGTACATCCACAACTGAGGCGAGACAGGCGAGAGGCGAGACAGGCTGGTGAAGCT 1080
Db 1046 TGTGAGTGGCTCAAGAGACCTTCTGAGAGGCGACAGCGCTGACAGCTGGTGAAGCT 1105
Qy 1081 GCGCTGAGAACTGGAGAGTGTAGCCCGGCTGAGTGTGAGTGTGACAGATGGAAGGC 1140
Db 1106 ACCGCTGAGAGCTGGAGAGCTTATCCCGACCGGAGTTCAGATGTGACAGAGCGAAAGGC 1165
Qy 1141 ACTGTCGAGGCGGACAGATGACATGCGCTGGTGTGAGAGGTGACAGAGCGGAGAC 1200
Db 1166 AGTGACTGGGCGGCGCAAACTCCCATGCTGTGCTCAAGAGAGTGCAGGAGCGCGCC 1225
Qy 1201 AGGACCTTACAGCTTCCGCGCTGGAGACTCCGCTGTGGCTGAGGCGCAATCAGCT 1260
Db 1226 AGGAGTCTACACTTCCGCTGTGGAGACTCTGAGAGTGTGAGGCGCAATCAGCT 1285
Qy 1261 GAGAGTGTGAGAGTGTGTAGGCGGCGAGATACATGAGAGAGAGGCTGTCTCCCGACAT 1320
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Qy 1321 GAGAGTGTGAGAGTGTGTAGGCGGCGAGATACATGAGAGAGAGGCTGTCTCCCGACAT 1380
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Qy 1381 GAGAGTGTGAGAGTGTGTAGGCGGCGAGATACATGAGAGAGAGGCTGTCTCCCGACAT 1440
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Db 1466 GAGAGTGTGAGAGTGTGTAGGCGGCGAGATACATGAGAGAGAGGCTGTCTCCCGACAT 1525
Qy 1501 GAGAGTGTGAGAGTGTGTAGGCGGCGAGATACATGAGAGAGAGGCTGTCTCCCGACAT 1560
Db 1526 GAGAGTGTGAGAGTGTGTAGGCGGCGAGATACATGAGAGAGAGGCTGTCTCCCGACAT 1585
Qy 1561 GAGAGTGTGAGAGTGTGTAGGCGGCGAGATACATGAGAGAGAGGCTGTCTCCCGACAT 1620
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Qy 1621 GAGAGTGTGAGAGTGTGTAGGCGGCGAGATACATGAGAGAGAGGCTGTCTCCCGACAT 1680
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Qy 1741 GAGAGTGTGAGAGTGTGTAGGCGGCGAGATACATGAGAGAGAGGCTGTCTCCCGACAT 1800
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Qy 1801 GAGAGTGTGAGAGTGTGTAGGCGGCGAGATACATGAGAGAGAGGCTGTCTCCCGACAT 1860
Db 1826 GAGAGTGTGAGAGTGTGTAGGCGGCGAGATACATGAGAGAGAGGCTGTCTCCCGACAT 1885
Qy 1861 GAGAGTGTGAGAGTGTGTAGGCGGCGAGATACATGAGAGAGAGGCTGTCTCCCGACAT 1920
Db 1886 GAGAGTGTGAGAGTGTGTAGGCGGCGAGATACATGAGAGAGAGGCTGTCTCCCGACAT 1945
Qy 1921 GAGAGTGTGAGAGTGTGTAGGCGGCGAGATACATGAGAGAGAGGCTGTCTCCCGACAT 1980

Db 1946 GAGAGTGTGAGAGTGTGTAGGCGGCGAGATACATGAGAGAGAGGCTGTCTCCCGACAT 2005
Qy 1981 GAGAGTGTGAGAGTGTGTAGGCGGCGAGATACATGAGAGAGAGGCTGTCTCCCGACAT 2040
Db 2006 GAGAGTGTGAGAGTGTGTAGGCGGCGAGATACATGAGAGAGAGGCTGTCTCCCGACAT 2065
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Qy 2101 GAGAGTGTGAGAGTGTGTAGGCGGCGAGATACATGAGAGAGAGGCTGTCTCCCGACAT 2160
Db 2126 GAGAGTGTGAGAGTGTGTAGGCGGCGAGATACATGAGAGAGAGGCTGTCTCCCGACAT 2185
Qy 2161 GAGAGTGTGAGAGTGTGTAGGCGGCGAGATACATGAGAGAGAGGCTGTCTCCCGACAT 2220
Db 2186 GAGAGTGTGAGAGTGTGTAGGCGGCGAGATACATGAGAGAGAGGCTGTCTCCCGACAT 2245
Qy 2221 GAGAGTGTGAGAGTGTGTAGGCGGCGAGATACATGAGAGAGAGGCTGTCTCCCGACAT 2280
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Qy 2281 GAGAGTGTGAGAGTGTGTAGGCGGCGAGATACATGAGAGAGAGGCTGTCTCCCGACAT 2340
Db 2306 GAGAGTGTGAGAGTGTGTAGGCGGCGAGATACATGAGAGAGAGGCTGTCTCCCGACAT 2365
Qy 2341 GAGAGTGTGAGAGTGTGTAGGCGGCGAGATACATGAGAGAGAGGCTGTCTCCCGACAT 2400
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Qy 2461 GAGAGTGTGAGAGTGTGTAGGCGGCGAGATACATGAGAGAGAGGCTGTCTCCCGACAT 2520
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Qy 2641 GAGAGTGTGAGAGTGTGTAGGCGGCGAGATACATGAGAGAGAGGCTGTCTCCCGACAT 2700
Db 2666 GAGAGTGTGAGAGTGTGTAGGCGGCGAGATACATGAGAGAGAGGCTGTCTCCCGACAT 2725
Qy 2701 GAGAGTGTGAGAGTGTGTAGGCGGCGAGATACATGAGAGAGAGGCTGTCTCCCGACAT 2760
Db 2726 GAGAGTGTGAGAGTGTGTAGGCGGCGAGATACATGAGAGAGAGGCTGTCTCCCGACAT 2785
Qy 2761 GAGAGTGTGAGAGTGTGTAGGCGGCGAGATACATGAGAGAGAGGCTGTCTCCCGACAT 2820
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[illegible][illegible]

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 Qy 2260 GGTACGCTGAGGCTGAGAGGCTCCGAGAGTAAGGGACCATGAGAGTGTGCTTCTC 2419
 Db 2241 GGTACGCTGAGGCTGAGAGGCTCCGAGAGTAAGGGACCATGAGAGTGTGCTTCTC 2400
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RESULT 14
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 DEFINITION Rattus norvegicus receptor tyrosine kinase VEGFR-3 (Vegfr3) mRNA, complete cds, alternatively spliced.
 ACCESSION AF402786
 VERSION AF402786.1 GI:16033529
 KEYWORDS
 SOURCE Rattus norvegicus.
 ORGANISM Rattus norvegicus.
 Rattus norvegicus: Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 REFERENCE 1 (bases 1 to 4254)
 AUTHORS Krishnan, J. and Sleeman, J. P.
 TITLE Characterization of a novel alternatively spliced form of VEGFR-3
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 4254)

[illegible]

OY	2650	GAAGCCTCCGCTTTCGGCATCCACAAAGGACACACTGTACACCGTGGCCGTGAAATAG	2659
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OY	2660	CTGAAGAAGGGCCGACGGCCAGCGACACCGCGCTGATGTGGAGCTCAAGATCTTC	2719
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OY	3620	CAGGTGTCCACCATGGCCCTTCACATCGTCCTCAGGTACAGCTTAGAGAGCGCCCGCAACG	3679
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FEATURES
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ACCESSION  X83287
VERSION    X83287.1 GI:619865
KEYWORDS   growth factor; receptor; Querk2 gene.
SOURCE     common quail.
ORGANISM   Coturnix coturnix
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            Phasianinae; Coturnix.
REFERENCE  1 (bases 1 to 4617)
AUTHORS   Eichmann,A., Marcelle,C., Bryant,C. and Le Douarin,N.M.
TITLE      Molecular cloning of Querk 2 and 2' two quail vascular endothelial
JOURNAL    Gene 174 (1): 3-8 (1996)
MEDLINE    9701727
PUBMED     8863722
REFERENCE  2 (bases 1 to 4617)
AUTHORS   Marcelle,C.A.
TITLE      Direct Submission
JOURNAL    Submitted (02-DEC-1994) C.A. Marcelle, Univ. of California, Irvine,
            Dept. of Developmental and Cell Biology, Irvine, California 92717,
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FEATURES
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Db 103 GCGAGTGTGTGAGAGCTATTTATGACCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 162
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[illegible]

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Db	1660	CAGGAGGCCAATCTCTGAGGCATGTAAATATATATGCTCTAAACCAAGTGGGTGGAT	1719
OY	1649	GAGGGCTCATCTACTTCTATATGTACCACCATCCCGACGCTTCACATCCATATCCAG	1708
Db	1720	GAGCGCTCATCTACTTCTATATGTACCAACCATTCACATGATTTGATGTCAATCTCAG	1779
OY	1709	CCATCCGAGAGACTACTAGAGGCGACGCGGTGGTCTCGACTGCCAAGCGCAAGTATC	1768
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OY	1769	AACTACAGACATCTGCGGTGTACCCCTCAACCTGTCCACGCTGCACGATGTGTACGGC	1828
Db	1840	ACCTACGACAACTCTGCAATGGTATGCTCTGAAACCTTTCCAAAGCTCCACGATAGAGAGGC	1899
OY	1829	AACCCCTTCCTGCTGATGCAGAAAGTGCATGCTTGGCGACCCCTGTGGCGCCGACG	1888
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OY	1889	CTGGAGAGGTGGCACCTGGGGCGCGCCACGCTCAGCCTGAGTATCCCTGCGCTC	1948
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OY	1949	GCGCCCGACACGAGGCGACCTGTGTGCGGAAGTGCACAAACGCGGCGACCATACAG	2008
Db	2017	TCCCTGGCGAGAGGAGGACATATGTGTAGGTGGACGAACGAGAAACCCGGAGAA	2076
OY	2009	CACCTGCCACAAAGATACCTGTGGGTGCAGGCGCTCGAAGCCCTCGGCTGCACGAGAC	2068
Db	2077	CACCTGCCACAAAGAAATACATCTCTGTGCGAGCGCTTCGAGATCCCGGCTCAAGCAGAC	2136
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OY	2189	GTCGACTTGGCGACTCCAAACCAAAAGCTGAGCATCCACGCGCTGGCCGACGAGATCGG	2248
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OY	2249	GCACGCTATCTGTGACAGTGTGCACAGCGCAAGGCTGCGTCAAACTCTGCGCGAGGTG	2308
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OY	2309	GCCGTGAAAGGCTCGGAGAGATAAGGCGAGCATGAGATGATGCTTGTGGTATCCGCGC	2368
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OY	2369	GTCATCGCTGCTTCTTCTGGGTCTCCCTCCCTCATCTTCTGTAAACATGAGAGCGCG	2428
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OY	2429	GCCACGACGATATCAAGAGGCGCTACCTGTGCATCATATGACCCCGGAGAGTGGCT	2488
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Db	2557	TTGGAGAGGACGTGGGCTACCTGCGCTATGATATTCAGCAAGTGGGATTTCCACAGAAC	2616
OY	2549	CGGCTGCACCTGGGAGAGAGTGTCTGGCTTACGCGCTTTCGGAAAGGTGTGGACCTCC	2608
Db	2617	CGGCTGCCTGGTAAAGTCTGGGTACATGTGTGCTTTGGAAAGGGGTGGAACTTCA	2676
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 QY 2909 GTGGAGCTGGCAAGCTGGA---TCGGAGGCGGCGGGGAGCGAGCGACAGGCTCTCTC 2965
 Db 2977 GTGGAGGAGTGAAGAGCGAGAGAGAGAGATGCTGTGGAGCTGATGACAGTATCTTC 3036
 QY 2966 GCGCGGTTCTTCGAAGCTGAGCGGAGCGAGCGAGCGGCGCTCTCCAGACCAAGAGCTGAG 3025
 Db 3037 AACGCTTTCTGATGAGCAAGAGCGAGAGCTGAG---CCAAATCCAGGAAGTGGAT 3090
 QY 3026 GAGCTGTGAGCTGAGCGCGGCTGACCTGGAATATCTTCTGTGCTACAGCTTCCAGTGGCC 3085
 Db 3091 GAGCTGTGAGCAAGTCTCTTGAAGTGAAGAGAGAGCTGATGCTTCCAGTGGCA 3150
 QY 3086 AAGGAGTACGATCTCTGCTTCCGAAGTGAATCCAGAGAGAGCTGGCTGTGGAGAC 3145
 Db 3151 GATGCTGTGAGCAAGTCTCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3210
 QY 3146 ATTCTGTGCTGAGAAATGACGCTGATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3205
 Db 3211 ATCTGTGCTGAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3270
 QY 3206 TACGAAGAGCTGACAGCTGCGCAAGGAGTGTGGGCTGAGCTGAGTGGATGGCC 3265
 Db 3271 TACGAAGAGCTGACAGCTGCGCAAGGAGTGTGGGCTGAGCTGAGTGGATGGCC 3330
 QY 3266 CCTGAAGAGCTGACAGCTGACAGGAGTGTGGGCTGAGCTGAGTGGATGGCC 3325
 Db 3331 CCGAGAGAGCTGCTTGAAGAGTGTGGGCTGAGCTGAGTGGATGGCC 3390
 QY 3326 CTCTCTGAGAGATCTCTCTGAGGAGCTGAGCTGAGTGGATGGCC 3385
 Db 3391 CACTCTGAGAGATCTCTCTGAGGAGCTGAGCTGAGTGGATGGCC 3450
 QY 3386 GAGTCTGAGAGAGCTGAGAGAGTGTGGGCTGAGCTGAGTGGATGGCC 3445
 Db 3451 GAGTCTGAGAGAGCTGAGAGAGTGTGGGCTGAGCTGAGTGGATGGCC 3510
 QY 3446 GCGATACCGAGCTGAGAGAGTGTGGGCTGAGCTGAGTGGATGGCC 3505
 Db 3511 GAAATTTACCGAGTGTGGGCTGAGCTGAGTGGATGGCC 3570
 QY 3506 TCGAGAGCTGAGAGATCTCTGAGGAGCTGAGCTGAGTGGATGGCC 3565
 Db 3571 TCGAGAGCTGAGAGATCTCTGAGGAGCTGAGCTGAGTGGATGGCC 3627
 QY 3566 GAGTCTGAGAGAGCTGAGAGAGTGTGGGCTGAGCTGAGTGGATGGCC 3625
 Db 3628 AAGGATTTACCGAGTGTGGGCTGAGCTGAGTGGATGGCC 3687
 QY 3626 TCGAGAGCTGAGAGATCTCTGAGGAGCTGAGCTGAGTGGATGGCC 3685
 Db 3688 CTTCTGAGAGAGATTTGAGATGAAGAGCTTGGATGGCC---AGGATAGCT 3741
 QY 3686 CCGCAGAGCTGAGAGAGTGTGGGCTGAGCTGAGTGGATGGCC 3745

Db 3742 TGTACAGCTTACGAGCAAGATATTACAGCTGCTGTGTTCCCTGGTGTGTTGAGCGGA 3801
 QY 3746 GGGGCTGAGAGCCCTGCTTCCCGAGATGAAGAGATTTGAGAGATTTCCCATGACCCA 3805
 Db 3802 GGAATTCAGATCAGTGTGCTTCCATGAGATTAAGAGATTTCCCATGAGACAT 3861
 QY 3806 ACGACCTCAAAAGCTCTGTGAGCAACGAGAGAGAGTGGATGGTGGCTGGAG 3865
 Db 3862 ACATATGTACAAAGGACACCGCGCAATTCAGAGAGAGTGGATGGTGGCTGGAG 3921
 QY 3866 GAGTTGAGCAGATAGAGAGAGCATAAGCAAGAAAGCGCTTCAAGCTGTAAAGAGCT 3925
 Db 3922 GAATTTGAGAGATAGAAAAACGACAGAAAGAGTGGATTTCAAGAGCAAAAGGCGC 3981
 QY 3926 GCGCAATGTGCTGTGAGCAGAGGATACCTGACTTCCAAAGGAGCGCGGCT 3985
 Db 3982 AACCGAGCTGGGAGCTGTGAGCAGAGAGTGTGAGCTGCGGAGAGATGTGCGCGTCA 4041
 QY 3986 GAGCGGAGGCGCGAGAGGCGAGTGTGTTACAAAGCGAGATAGGAGAGCTGTGAG 4045
 Db 4042 TACGATCCCGAGTGGAGGCGAGCTTTTACAAAGTGAATAGGAGAGCTGTGAG 4101
 QY 4046 CCAAGCAGAGAGAGCAGCTGCTCCCGTGTG 4077
 Db 4102 CACTCTGAGAGAGCGAGCTGACACCCCGC 4133

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